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us-10-600-230-1.rge

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: December 28, 2005, 08:02:56 ; Search time 2756 Seconds
(without alignments)
10003.292 Million cell updates/sec

Title: US-10-600-230-1
Perfect score: 485
Sequence: 1 gcgcgcggaaggaggaaagt.....cctccaaatgatgaggtacc 485
Scoring table: IDENTITY\_NUC
Gapop 10.0 , Gapext 1.0

Searched: 5883141 seqs, 28421725653 residues
Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:\*
1: gb ba:\*
2: gb in:\*
3: gb env:\*
4: gb on:\*
5: gb ov:\*
6: gb pat:\*
7: gb pat:\*
9: gb r:\*
9: gb r:\*
10: gb sts:\*
11: gb sy:\*
11: gb sts:\*
13: gb v:\*
14: gb htg:\*
15: gb pl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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	9.9	10.0	10.1	10.3	10.4	10.6	10.6	10.6	10.6	10.6	10.8	13.0	39.3	58.6	59.3	92.0	97.9	97.9	Match	de
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	BX119907	AC095377	CR854985	AC163463	AC124696	AC087277	AC124497	AC123054	AC079954	BV061001	CR382399	CR380948_4	SCYBR023C	YSCPCHSY	AY557705	SCYBR022W	SCGAL1	SCAL1	ID	
	BX119907 Zebrafish	AC095377 Rattus no	CR854985 Danio rer	AC163463 Bos tauru	AC124696 Mus muscu	AC087277 Homo sapi	AC124497 Mus muscu	AC123054 Mus muscu	AC079954 Homo sapi	BV061001 S212P6318	CR382399 Plasmodiu	Continuation (5 of	Z35892 S.cerevisia	M73697 S.cerevisia	AY557705 Saccharom	Z35891 S.cerevisia	X76078 S.cerevisia	X57300 Saccharomyc	Description	

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44 d 07 d	4.	45	45.2	45.2	45.2	45.4	•	45.4	45.6	45.6	45.6	46	46	46	46.2	46.2	46.4	46.4	46.6	46.6	46.6	47	47	47.2	47.2	47.4
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BX537162	CR749178	AX458482 Sequence	CR383681	CR407564 Danio rer	BX293540 Zebrafish	AC023534 Homo sapi	AL928920	AC158414 Pongo pyg	AC155816 Mus muscu	AC122434 Mus muscu	BX247871 Zebrafish	AL929355 Plasmodiu	AE014827 Plasmodiu	AE014835 Plasmodiu	AX251775 Sequence	AX345620 Sequence	CR456634 Macropus	AC099738 Homo sapi	CR847971 Danio rer	AC132600 Mus muscu	BX842571 Zebrafish	AC005036 Homo sapi	AY701231 Orconecte	CR376799 Danio rer	AL402311 T3 end of	

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## ALIGNMENTS

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CDS	promoter	FEATURES source	TITLE JOURNAL	REFERENCE	JOURNAL	REFERENCE AUTHORS TITLE	ORGANISM	ACCESSION VERSION KEYWORDS SOURCE	RESULT 1 SCAL1 LOCUS DEFINITION
/gene="CAL1" 2793578 2793578 /gene="CAL1" /EC_number="2.4.1.16" /codon_start=1 /evidence=experimental			Direct Submission Submitted (16-JAN-1991) A. Duran, Instituto de Microbiologia Bioquimica, Facultad de Biologia, CSIC/Universidad de Salamanca, 37008 Salamanca. Spain	2 (bases 1 to 4046) Duran, A.	Dmyces cerevisiae Biol. 114 (1), 101-109 (1991)	1 (bases 1 to 4046) Valdivieso,M.H., Mol.P.C., Shaw,J.A., Cabib,E. and Duran,A. CALI, a gene required for activity of chitin synthase 3 in	Saccharomyces cerevisiae  Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetales; Saccharomycetaceae; Saccharomyces.	X5/300 X57300.1 GI:3359 CALl gene; chitin synthase 3. Saccharomyces cerevisiae (baker's yeast)	SCAL1 SCAL1 4046 bp DNA linear PLN 02-AUG-1991 Saccharomyces cerevisiae CAL1 gene for chitin synthase 3.

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DEFINITION
ACCESSION
VERSION
                                                                                                                                                                                                           RESULT 2
SCGAL1/c
LOCUS
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                                                                                                                                   S.cerevisiae (alphaS288C) GAL1, X76078
X76078.1 GI:498748

CAL1 gene; chitin synthase 3; FUR4 gene; GAL1 gene; galactokinase; ribosomal protein L2B; uracil permease; YBR0304 gene; YBR0308 gene; YBR0310 gene; YBR0312 gene; YBR0313 gene; YBR0314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TGTATAATTCAAAATACTTTGCTTTTCTCCATGACTTGAACCTCCAAATGATGAGGTA 483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ACTIGITCGAGITITGCTTTTGCTTCTCTAAAGGTCTTCAATTTATCTAAAGCAAGTTT 425
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NRKEESDSFVA"
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PUBMED
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AUTHORS
TITLE
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Saccharomyces cerevisiae (baker's yeast)
Saccharomyces cerevisiae
Saccharomyceta; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
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Submitted (11-NOV-1993) P.H.M. Smits, University of Amsterdam, Section for Molecular Biology, Department of Molecular Cell Biology, Kruislaan 318, 1098 SM Amsterdam, NETHERLANDS
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 (bases 1 to 33117)
Smits,P.H.M., de Hann,M., Maat,C. and Grivell,L.A.
The complete sequence of a 33 kb fragment on the right arm of chromosome II from Saccharomyces cerevisiae reveals 16 open reading frames, five previously identified genes and a homologue of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Smits, P.H.M.
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RKFDLPLDGSYYTI DPSVSDWSNYFKCGLHVJAHSFLKKLAPERFASAPLAGLQVFCEG
DVPTGSGLSSAAF I CAVALAVVKANMGPGYHMSKQNLMFI I TVVAEHYVGVNNGGMDQ
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12594. .13499
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Local

Similarity

97.9%;

Score 474.8; DB 15; Pred. No. 1.8e-80; Mismatches

476;

Conservative

<u>..</u>

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Indels

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Gaps

7550

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7609

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7489

186

CTAAGGCAATTACAGCTGATATACTGTAAAACTCATGTCGCCACTAAATTCTTCTAACAC CTTAGAACTAAAACTTAATAAATAATATTCTCTATCTTTAAAGGCACATATTACGTGG CTTAGAACTAAAACTTAATAAATAATATTTCTCTATCTTTAAAGGCACATATTACGTGG

245 7430 185 7490 125

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306 TTTATATTCCCCTATTGGGTATTTGATGTGGCCGTTTAAATAGTCACCGATTGAATCTTC 365

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7310 305 7370 7549 ACTTACAAGTTGATATATGGTTGTGTATATTTATTTTGAGAGGTATTTTAACACAC

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LPSGSSKGDLKLGDRVIPLOARQGTWSNYRVPSSSSDLIKNXDLDIFSAATVSVNYTEN
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CDS	o e	TITLE JOURNAL PUBMED REFERENCE AUTHORS JOURNAL I	RESULT 3 SCYBRO22W/C LOCUS DEFINITION S ACCESSION Z VERSION Z VERSION Z ORGANISM S ORGANISM S REFERENCE 1 AUTHORS F	Db 7309 Qy 366 Db 7249 Qy 426 Db 7189
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                                                                                                                                                                                                                                                                                                                                                                                                                                   447; Conservative
                                                                                                                                                             849
                                                                                                                                  336
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                                                                                                                         GCCGTTTAAATAGTCACCGATTGAATCTTCACTTGTTCGAGTTTTGTCTTTTTGCTTCTCT 395
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0; Mismatches 1
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ACCESSION VERSION KEYWORDS SOURCE ORGANISM RESULT 4 AY557705/c LOCUS REFERENCE AUTHORS JOURNAL REFERENCE AUTHORS DEFINITION COMMENT TITLE JOURNAL TITLE AL Unpublished
CE 2 (bases 1 to 534)
CE 2 (bases 1 to 534)
RS Marsischky,G., Rolfs,A., Richardson,A., Kane,M., Baqui,M.,
RS Marsischky,G., Rolfs,A., Richardson,A., Kramer,J., Moreira,D.,
RS Marsischky,G., Vannberg,F., Weger,J., Kramer,J., Moreira,D.,
Taycher,E., Lu,Y., Vannberg,F., Weger,J., Kramer,J., Williamson,J.,
Kelley,F., Zuo,D., Raphael,J., Hogle,C., Jepson,D., Williamson,J.,
Camargo,A., Gonzaga,L., Vasconcelos,A.T., Simpson,A., Kolodner,R.,
Harlow,E. and LaBaer,J.
Direct Submission
AL Direct Submission
AL Submitted (17-FEB-2004) Biological Chemistry and Molecular
Pharmacology, Harvard Institute of Proteomics, 320 Charles St.,
Cambridge, MA 02141, USA
This clone is part of a collection of Saccharomyces cerevisiae
full-length ORF clones generated by the Harvard Institute of Saccharomyces cerevisiae (baker's yeast)
Saccharomyces cerevisiae
Saccharomyces cerevisiae
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.

1 (bases 1 to 534)
Marsischky,G., Rolfs,A., Richardson,A., Kane,M., Baqui,M.,
Taycher,E., Hu,Y., Vannberg,F., Weger,J., Kramer,J., Moreira,D.,
Taycher,E., Zuo,D., Raphael,J., Hogle,C., Jepson,D., Williamson,J.,
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Harlow,E. and LaBaer,J.
Harlow,E. and LaBaer,J.
Creation of the YFLEX clone resource: cloning of Saccharomyces
cerevisiae ORFs in the Gateway recombinational cloning system AY557705 534 bp DNA linear PLN 14-MAR-2004 Saccharomyces cerevisiae clone FLH000707.01X YBR022W gene, complete AY557705.1 GI:452 Yeast ORF Project. GI:45269300

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REFERENCE
AUTHORS
TITLE
                                                                                                                                                                                                                                                                                                                                                              SOURCE
ORGANISM
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                                                                                                                                                                                                                                                                       M73697.1 GI:172103
chitin synthase.
Chitin synthase.
Saccharomyces cerevisiae (baker's yeast)
Saccharomyces cerevisiae
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetales; Saccharomycetales
                              CSD2, CSD3, and CSD4, genes required for chitin synthesis i Saccharomyces cerevisiae: the CSD2 gene product is related chitin synthases and to developmentally regulated proteins Rhizobium species and Xenopus laevis
MOL. Cell. Biol. 12 (4), 1764-1776 (1992)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         S.cerevisiae CSD2 gene complete cds.
M73697
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Proteomics. Each CDS has been cloned with its native stop-codon. The CDS has been directionally cloned using the Gateway cloning system into the donor vectors pDONR 201 or pDONR 221. Additional sequences in the clone: 'TCCAGCTGACCACC' after the attil site and before the 'ATG' (from Research Genetics primers used to amplify
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               the ORFs, including a Kozak consensus sequence);
'ATCCCCGGGAATTGCCATG' after the stop codon and before the attL2
site (from the Research Genetics primers used to amplify the ORFs)
                                                                                                                                                                                 Bulawa, C.E.
CSD2, CSD3,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AGTITTGTCTTTTGCTTCTAAAAGGTCTTCAATTTATCTAAAGCAAGTTTTGTATAATT
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/db_xref="GI:45269301"
/translation="MSNITYVKGNILKPKSYARILIHSCNCNGSWGGGIAYQLALRYP
/translation="MSNITYVKGNILKPKSYARILIHSCNCNGSWGGGIAYQLALRYP
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LALDKLKTFREAKDKTRTSEDSIGDYLNGHIKYPIGEYKLEMPQINSGIFGVPWKETE
RVLEEFSGDWSFTVYQL"
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/mol_type="genomic DNA"
/mb xref="taxon: 4932"
/clone="FLH000707.01X"
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DEFINITION ACCESSION

SCYBR023C S.cerevisiae chromosome Z35892 Y13134

5176 bp II reading

DNA linear I frame ORF YBR023c.

PLN 11-AUG-1997

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CGGAAGGAGAAAGTGACTCCTTCGTTGCGTAGACAGTATGAAAATATTTTTACTGTGAT
                                                                                                                                            GCGTTCTGTCTCTTTCCAAGGGACTCCGAATATGCCACTATTTATCTGT
                                                                                                                                                                                                                                                                                                                              CTTAGAACTTAAATAATAAATAATTACTCTATCTTTAAAGGCACATATTACGTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GCGTTCTGTCTCTTTCCAAGGGACTCCGAATATGCCACTATTTATCTGT 4345
                                                                                                                                                                                                                      TTAAGGCAATTACAGCTGATATACTGTAAAACTCATGTCGCCACTAAATTCTTCTAACAC
                                                                                                                                                                                                                                                                    CTAAGGCAATTACAGCTGATATACTGTAAAACTCATGTCGCCACTAAATTCTTCTAACAC
                                                                                                                                                                                                                                                                                                                                                                                    CTTAGAACTAAAACTTAATAAATAATATTTCTCTATCTTTAAAGGCACATATTACGTGG
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ERSHLNNPDNEHFYYAQKTOBOMNHLDVLPSSTGVNPNATRRSGSLRSKGSVRSKESG
RETDSYLAQDMNTTDKKASVKI SDGGVABDEPDDDVDNEESS TOP1NKS I KPLRK
ETNDYLSFWQMYCYF I TFWAPAP I LAFCGMPKKGRQWAWREKVALI SVILYI GAAI VAF
ETTROFTLSFWQMYCYF I TFWAPAP I LAFCGMPKKGRQWAWREKVALI SVILYI GAAI VAF
ETTROFTKSFWQMYCYF I TFWAPAP I LAFCGMPKKGRQWAWREKVALI SVILYI GAAI VAF
ETTROFTKSFWQMYCYF I TFWAPAP I LAFCGMPKKGRQWAWREKVALI SVILYI GAF
UFARAWNCHTSKEDRDAFYGLKSKADVYFTWDGI KNUSSRNLI YVNGDVLDLDLLDWL
SDAGKDASFLFQNVNGCHNLI TFPKSNS I PHDDDNNLAWYFPCKLKNQDGSSKENFT
VENYAGWNCHTSKEDRDAFYGLKSKADVYFTWDGI KNUSSRNLI YVNGDVLDLDLLDWL
EXDDVDYFVVFDDLKTSNLQGYDLSLVLSNCHBERK LARCLSEI I KVGEVDSKTVGCI A
SDVVLYVSLVF I LSVVI I KF I I ACYFRWTVAKQKAY I VDNKTMDKTMDKTTND I EDWSNN I
QTKAPLKEVDPHLRFKKYSKESJGHKRAST FDLLKKAYSSKMFQNESV I DLDTSWSSS I
QSLOSTYSTEVENTOWOWN LSNENKAVHSNAPSTLLFTSSMFWNKATSS PVPGSSLI
QSLDSTI I HPDI VQQPPLDFMPYGFPLI HTI CFVTCYSEDEEGLRTTLDSLSTTDYPN
SHKLLMVVCDGL I KGSGNDKTTPBI ALGMMDDFVTPPDBVKPYSTVAVASGSKRHWMA
KI YAGFYKNDDSTI PPENQQRVPI I TIVKCGTPAEGCAAKFGNRGKRBSQI I LMSETLE
KITPDERMTQLEFQLLKNI WQI TGLMADFYETVLMVDADTKVPPDALTHNVAEMVKDF
LIMGLGGETKI ANKAQSWVTALQVFSYY I SHIQAKAFESVFGSVTCLPGCFSMYRI KS
PKGSDGYWPVLANDFU VERYSDDNINTTLHKKNLLLLGERGENEFLSSLEMLKTFFKRRQVF
ENGSDGYWPVLANDFU VERYSDDNINTTLHKKNLLLLLGERGENEFLSSLEMLKTFFKRRQVF
ENGSDGYWPVLANDFU VERYSDDNINTTLHKKNLLLLLGERGENEFLSSLEMLKTFFKRRQVF
ENGSDGYWPVLANDFU VERYSDDNINTTHKKNLLLLLGERGENEFLSSLEMLKTFFKRRQVF
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GTMVLPLAICFTIYVIIFAIVSKPTPVITLVLLAIILGLPGLIVVITATRWSYLWWMC
VYICALPIWNFVLPSYAYWKFDDFSWGDTRTIAGGNKKAQDENEGEFDHSKIKWRTWR
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/function="Required for chitin synthesis in vivo and for chitin synthase Illactivity in vitro."
/note="'Deduced amino acid sequence of CSD2 has limited, butstatisticallysignificant similarity to chitin synthases, to the nodC protein of Rhizobiumand to the DG42 protein of X. laevis'; putative"
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/db_xref="GI:172104"
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/protein_id="AAA34844.1"
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/mol_type="genomic DNA"

/db_xref="taxon:4932"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 284.2; DB 1
Pred. No. 3.4e-44;
0; Mismatches 3
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GI:536229

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VERSION
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AUTHORS
JOURNAL
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ORGANISM
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JOURNAL
PUBMED
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TITLE
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Brendel, M., Brueckner, M., Bussereau, F., Christiansen, C.,
Contreras, R., Crouzet, M., Cziepluch, C., Demolis, N., Delaveau, T.,
Contreras, R., Crouzet, M., Cziepluch, C., Demolis, N., Delaveau, T.,
Doignon, F., Domdey, H., Duesterhus, S., Dubois, E., Dujon, B., El
Bakkoury, M., Entian, K.D., Feuermann, M., Fiers, W., Fobo, G.M.,
Pritz, C., Gassenhuber, H., Glansdorff, N., Goffeau, A., Grivell, L.A.,
de Haan, M., Hein, C., Herbert, C. Jonniaux, J.C., Kallesoe, T.,
Jacq, C., Jacquet, M., Jauniaux, J.C., Jonniaux, J.L., Kallesoe, T.,
Kiesau, P., Kirchrath, L., Koetter, P., Korol, S., Liebl, S., Loghe, M.,
Kiesau, P., Kirchrath, L., Koetter, P., Korol, S., Liebl, S., Loghe, M.,
Kiesau, P., Messenguy, F., Miosga, T., Molemans, F., Mueller, S.,
Nasr, F., Obermaler, B., Perea, J., Pierard, A., Piravandi, E.,
Nasr, F., Obermaler, B., Perea, J., Pierard, A., Piravandi, E.,
Pohl, F.M., Pohl, T.M., Potier, S., Proft, M., Purnelle, B., Ramezani
Rad, M., Rieger, M., Rose, M., Schhaff-Gerstenschlaeger, I.,
Schears, B., Schwarzlose, C., Skala, J., Slonimski, P.P.,
Scherens, B., Schwarzlose, C., Skala, J., Slonimski, P.P.,
Smits, P.H.M., Souciet, J.L., Steensma, H.Y., Stucka, R.,
Urresterazu, A., van der Aart, Q.J., van Dyck, L., Vassarotti, A.,
Vetter, I., Zagulski, M., Zimmermann, F.K., Mewes, H.W. and Kleine, K.
Complete DNA sequence of yeast chromosome II

AL EMBO J. 13 (24), 5795-5809 (1994)
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Saccharomyces cerevisiae
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Direct Submission
Submitted (30-AUG-1994) Data collected by MIPS on behalf of the European yeast chromosome II sequencing project. MIPS at the Max-Planck-Institut fuer Biochemie, Am Klopferspitz 18a D-82152 Martinsried, FRG; E-mail: Mewes@mips.embnet.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 (bases 1 to 5176)
Grivell,L.A., de Hann,M., Maat,M.J.
Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Saccharomycetales; Saccharomycetaceae; Saccharomyces.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (bases 1 to 5176)
LTFGFFYKTVCSSSKLRLKNNEVSTEFVVINGKAYELDTSSRSGLIQDVEVDSDTLYGPW
SDAGKDAS FLFQNVNGNCHNLITPKSNSS I FHDDDNNLAWYEFCKLKNQDGSSKPNFT
VENYAGMACHTSKEDROAFYGLKSKADVFTWGGI KNSSRNLI VYKURDVLDLLDLLD
EKDDVDYFVPEDDLKTSKLOVFTGLESVLVLSNGHERK I ARCLEB I I KVCBVDVLDVLDKTVGLIDA
EKDVLYVSLVFILSVVI I KFI I ACYFRWTVARKQGAY I VDNKTMDKHTND I EDWSNNI
GYKAPLKEVDDHLR PKKYSKSLGHKAASTFDLLKKHSSKMFGNESV I DLDTSMSSS
LQSSGSYRGMTTMTTQNAWKLSNENKAVHSRNPSTLLFTSSMFWNKATSVEVESVLI
QSLGSTI I HPDI VQQFPLDFMFYGFFLHTI CEVTCYSSDEEGLATTLDSLSTUDYBN
SHKLLMVCDGL I KGSGNDKTTPE I ALGMMDDFVTP DDEVKFYSYVAVASGSKRHNMA
KI YAGFYKYDDSTI PPENQQRVFI I TI VKCGTPAEGGAAKFGNGKRDSQI I LMSFLE
KI PROFEDERUM I EDGI V DATHAMAD
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/proteIn_id="CAA84965.1"

/proteIn_id="CAA84965.1"

/db_xref="GG1:536230"

/db_xref="GG1:536230"

/db_xref="GG1:536230"

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/db_xref="MTGLNGDDPDTYLINLNODEESILRSRHSVGSGAPHROGSLVRP

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/translation="MTGLNGDDPDMYLINLNODEESILRSRHSVGSGAPHROGSLVRP

/translation="MTGLNGDDPDMYLINLNODEESICHTRRSGSLRSKGSVRSKFSG

RETDSYLLOPMITDKKASVKLSDEGYAEDEFDKOGVVNREESSTQPINKSIKPLRK

ETNDTLSFWQNYCYFITFWARAPILAFGGMPKKEROMARREKVALISYILYGAIVAF

ETNDTLSFWQNYCYFITFWARAPILAFGGMPKKEROMARREKVALISYILYGAIVAF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gene="CHS3"
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DEFINITION ACCESSION VERSION

Plasmodium falciparum chromosome CR382399 AL844505 CR382399.1 GI:46361038

'n

complete sequence; segment

INV 17-APR-2005 ce; segment 2/5.

DNA

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RESULT 7
CR380948 4
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RESULT 8
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CR380948 0
CR380948 1
CR380948 2
CR380948 3
CR380948 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CGGAAGGAGGAAAGTGACTCCTTCGTTGCGTAGACAGTATGAAAAATATTTTTACTGTGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CTTAGAACTAAAACTTAATAAATAAATATTTCTCTATCTTTAAAGGCACATATTACGTGG 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CGGAAGGAGAAAGTGACTCCTTCGTTGCATAGACAGTATGAAAATATTTTTACTGTGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CTTAGAACTAAAACTTAATAAATAATATTTCTCTATCTTTAAAGGCACATATTACGTGG
                                                                                                                                                                                                              TTCCCCTATTGGGTATTTGATGTGGCCGTTTAAATAGTCACCGATTGAATCTTCACTTGT 371
                                                                                                                                                                                                                                                                       TGTCTCTTTCCAAGGGACTCCGAATATGCCACTATTTATCTGTGGCATTTCCAATTTATA 311
                                                                                                                                                                                                                                                                                                    CATTCAGAGTTCATACACAGTAAAATTCATAGATCTGTCATACTTCTTTAATACTTCCTC 31327
                                                                                                                                                                                     ATCCTTAAGTACTCCGCTCTTCAGTTTCAATAGTTTCTCAATTTCTTTATCAAGATTTGC 31447
                                                                                                                                                                                                                                            GGTTTCTGGCCAAGGGACTCCAAATATACCGCTATTGATTTTTGGCATCTCGAGCTTGTA 31387
                                                                                                                                                                                                                                                                                                                               CAATTACAGCTGATATACTGTAAAACTCATGTCGCCACTAAATTCTTCTAACACGCGTTC
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                                                                                                                                                            TCGA----
                                                                       AGTATAATCAACTATACTAGTGCCGCTGCCATGGCTCGCACCTCCAAATATTGATGTA 31565
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nilarity 53.4%;
Conservative
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VPKAACKTIAPDKFKVLLSQRRRWINSTVHNLFELVLIRDLCGTFCFSMQFVIGIELI
GTMVLPLAICFTIYVIIFAIVSKPTPVITLVLLAIILGLPGLIVVITATRWSYLWWMC
VYICALPIWNFVLPSYAYWKFDDFSWGDTRTIAGGNKKAQDENEGEFDHSKIKWRTWR
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/note="ARS-consensus"
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of CR380948
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Pred. No. 1.7e-26;
0; Mismatches 1
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Pred. No. 0.
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                                                                                                                                                                                                                                                                                                                                                              Mismatches 133;
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                                                                                                                                                                                                                                                                                                                                                                             0.0075;
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                                                                                                                                                                                                                                                                                                                                                                6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (26-MAR-2004) P.falciparum Genome Sequencing Consortium, The Welcome Trust Sanger Institute, Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SA, UK
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Cherevach, I., Davis, P., Goodhead, I., Stevens, K., Mungall, K.,
Berriman, M., Pain, A., Hall, N., Atkin, R., Chillingworth, C.,
Doggett, J., Ormond, D., Sanders, M., Hayes, R., Hall, S., Quail, M.
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Berrinan, M., Pain, A., Hall, N., Atkin, R., Chillingworth, C.,
Doggett, J., Ormond, D., Sanders, M., Hayes, R., Hall, S., Quail, M.
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Submitted (20-SEP-2002) P.falciparum Genome Sequencing Consortium,
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Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
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Plasmodium falciparum
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Center for Genome

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Matches 93
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                      BV061001 633 bp DNA linear : S212P6318FG5.TO CZECHII/Ei Mus musculus STS genomic,
tagged site
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                                                                                                                                                                                                                                                                                                   ATTTATTTGAGAGGTATTTTAACACCCTTAGAACTAAAACTTAATAATAATATTTCT 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                        ACAGTATGAAAATATTTTTACTGTGATACTTACAAGTTGATATATGGTTGTGTGTAACTT 98
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                                                                                                                                                                                                                                          CTATCTTTAAAGGCACATATTACGTGGCTAAGGCAATTACA 199
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Y I KMS I Y INMFLAKYYTY I NYKDMGIL KYLKGYQKR VMKQVEKI TENI YAVIMKSDVI
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QI KETNYNNQENHYSCKYNEGEEYYHNKP I NI I NSHHIE I KKKCYNEJ GOMI HEAD
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KI KESI I INLEFYRKVEKNINSYESKI Y EQLDVS I I FPULI THEOVRE ETTUTUTNINGT I GTWYF
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Matches 145
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eut
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
1 (bases 1 to 633)
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BV061001.1
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Location/Qualifiers
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WGS-discovery: Paired-end low-coverage whole genome shotgun reads
WGS-discovery: Paired-end low-coverage whole genome shotgun reads
were generated from 129S1/SvImJ, C3H/HeJ, and BALB/CByJ. The WGS
reads were placed uniquely on the MGSCv3 C57BL/6J assembly and SNI
detection was carried out by SSAHA-SNP. 225,000 reads were
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: kersli@genome.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Research
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Kerstin Lindblad-Toh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mus musculus (house mouse)
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Primer B: None
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GATATATGGTTGTGTGTAACTTATTTATTTGAGAGGTATTTTAACACACCTTAGAACTAA 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAGTGACTCCTTCGTTGCGTAGACAGTATGAAAATATTTTTTACTGTGATACTTACAAGTT 76
                                                                                                                                             CCTTCTCAATTTTACCCCTCCTTCAACCTCTTCCATTTGCCATTACCAGGTTCCATCACA 108
                                                                                                                                                                                                                                                     TAAATTAATATTTCTGAAAATTTTCTGGCATGTGTATTGTATTCACATCACTTTTACCCCT
                                                                                                                                                                                                                                                                                                        ACAGCTGATATACTGTAAAACTCATGTCGCCACTAAATTCTTCTAACACGCGTTCTGTCT
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                                    C 107
                                                                                                                                                                                                CTTTCCAAGGGACTCCGAATATGCCACTATTTATCTGTGGCATTTCCAATTTATATTCCC 316
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nilarity 48.2%;
Conservative
                                                                                             317
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REFERENCE AUTHORS TITLE TOURNAL REFERENCE AUTHORS TITLE TOURNAL REFERENCE AUTHORS TITLE	TITLE	REFERENCE AUTHORS	RESULT 10 AC079954 LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM
2 (bases 1 to 158785)  2 (bases 1 to 158785)  Worley, K.C.  Direct Submission  Submitted (20-SEP-2000) Human Geneme Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA  3 (bases 1 to 158785)  Worley, K.C.  Direct Submission  Submitted (01-MAY-2001) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA  4 (bases 1 to 158785)  Worley, K.C.  Direct Submission	Director, C. Burkett,C. Burkett,C. Cavazos,S. Chiu,D., Ch Ding,L., Ded Ding,L., Ded Ding,L., Ded Ding,S. Ford,J., F Garner,T., P., Hale,S. Huber,J., Huber,J., Kureshi Li.J., Li., Li.J., Li., H. Lozado neshwari,M. Mitchell,T. Moser,M. Mei,G., Marti Mei,G., Marti Mei,G., Marti Mery,G., Nguyen,N. N	Eutheria; Euarchontoglires; Primates; Cata; Homo. 1 to 158785) 1 to 158785) 2 to Adams, F.R., Adams, C., Adams, F.R., Banks, T., Banks, T., Banks, T., Banks, T., Banks, T., Banks, Blankenburg, K., Bonnin, D., Bou, Bimage, K., Blankenburg, K., Bonnin, D., Bou	158785 bp DNA 15 12 BAC RP11-179A1 (Roswel /) complete sequence. 3 GI:13899365 18 (human) Metazoa: Chordata: Craniata

REFERENCE AUTHORS TITLE REFERENCE AUTHORS TITLE JOURNAL COMMENT JOURNAL JOURNAL Submitted (07-MAR-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA 5 (bases 1 to 158785)

Worley,K.C.
Direct Submission
Submitted (25-JUL-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA 6 (bases 1 to 158785)
Worley,K.C.
Direct Submission Direct Submission
Submitted (19-MAR-2003) Human Genome Sequencing Center, Depar Submitted (19-MAR-2003) Human Genome Sequencing Center, Depar of Molecular and Human Genetics, Baylor College of Medicine, of Molecular and Human Genetics, USA
Baylor Plaza, Houston, TX 77030, USA
On May 1, 2001 this sequence version replaced gi:13877202.
INFORMATION: http://www.hgsc.bcm.tmc.edu/ or email gc-help@bcm.tmc.edu Department

CLONE LENGTH: This sequence does not necessarily represent the entire insert of this clone. Overlapping regions of clones are only sequenced and submitted once, so the sequence for the remainder of the insert may be found in the record for the adjacent clones. Overlapping clones are noted at the beginning and end of the Features listing.

ANNOTATION OF FEATURES:

STSs are identified using ePCR (Genome Res. 7:541-550) searches of a local database that includes entries from dbSTS, GDB, and local mapping efforts.

local mapping efforts.

Repeats are identified using RepeatMasker (A. Smit and P. Green, unpublished.) for Human and Mouse sequences.

Genes and Region of sequence similarity are identified by BLAST (Nuc. Acids Res. 25:3389-3402) similarity (expect < 1e-34) to the EST and cDNA sequences. Genes demonstrate at least two exons flanked by consensus splice sites that maintained sequence continuity across the splice junctions. Sequences that are not identical matches are annotated as similar.

SEQUENCING READ COVERAGE: Sequencing is completed to a minimum standard of double strand coverage with a minimum of 2 clones and 2 reads with no ambiguities or 2 chemistries with a minimum of 2 clones and 3 reads with no ambiguities. If the sequence quality for a region does not meet this standard, it will be indicated in the annotation as Low Coverage.

QUALITY OF INDIVIDUAL BASES: This sequence meets stringent quality strandards - estimated error rate less than 1 per 10,000 bases. Reports of lowest quality individual bases and measures of base quality are listed below. Description of the metrics can be found http://gc.bcm.tmc.edu:8088/quality.info/genbank.annotation.html.

QUALSTAT-REPORT-----

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ion	r of N's i	er of conse	ion of Phi	ige error i	) values ir	Contig length:	
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                                                                                                                                         TATGAAAATATTTTTACTGTGATACTTACAAGTTGATATATGGTTGTGTGTAACTTATTT
                                                                                  C-TCATAAACAAACAATGAGAGTTTTCTTTTATTGATGCTTTACTTCACTGCTACACTTT
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                                                      ATTTCAGAAATTTTGCTAAATTCAGTAAATCTGTAATTTATTATTCTAGGCATTCTTTAG
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tatgactaag (n) gaagtttacc
gcaccaatag (n) gaaggtcttca
aagtgcctca (n) aagcaaggtc
actccatctc (n) aagaaaaaa
gtattcctag (n) tttttttt
ctagmtcttt (n) tttttttt
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atttnggcaa (n) tagtatccaa
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cccactonnt (n) nnncaagaac
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Mus musculus BAC clone RP24-220N11 from
AC123054
AC123054.2 GI:22213530
HTG.
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Submitted (29-WAY-2002) Genome Sequencing Center,
Parkway, St. Louis, MO 63108, USA
S (Dases 1 to 174874)
McPherson, J.D. and Waterston, R.H.
Direct Submission
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parkway, St. Louis, MO 63108, USA
4 (bases 1 to 174874)
McPherson, J.D. and Waterston, R.H.
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Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
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McPherson, J.D. and Waterston, R.H.
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             Contact: submissions@watson.wustl.edu
                                            Center: Washington University Genome Sequencing Center Center code: WUGSC Web site: http://genome.wustl.edu
Center project name: M_BB0220N11
                                                                                                                                                                                                         (13-AUG-2002) Genome Sequencing Center, St. Louis, MO 63108, USA
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NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by
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This sequence is the entire insert of the clone.
Location/Qualifiers
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/mol_type="genomic DNA"
/db_xref="taxon:10090"
/chromosome="5"
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Mus musculus
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eut
Eukaryota; Metazoa; Chordata; Craniata; Glires; Rodentia;
Mammalia; Butheria; Buarchontoglires; Glires; Rodentia;
Sciurognathi, Muroidea; Muridae; Murinae; Mus.
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Mus musci
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4 (bases 1 to 206926)
McPherson, J. D. and Waterston, R.H.
Direct Submission
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Submitted (29-JAN-2003)
                                                                                                              Parkway, St. Louis, MO 63108, USA 5 (bases 1 to 206926) McPherson, J.D. and Waterston, R.H.
                                                                                                                                                                                                                                                              3 (bases 1 to 206926)
McPherson, J.D. and Waterston, R.H.
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Unpublished (2001)
                                                                                                                                                                                                                                                                                                                        Wilson, R.
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University, 4444 Forest
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Department of Genetics,
Park Avenue, St. Louis,
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COMMENT
NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.
                                                                                                                                                                                                                                                                                                                                                                                                                            On Jan 29, 2003 this sequence version replaced gi:25450603
                                                                                                                                                                                                                                               Web site: http://genome.wustl.edu
Contact: submissions@watson.wustl
Summary Statistics
                                                                                                                                                                                                                     Center project name: M_BA0480E08
                                                                                                                                                                                                                                                                                                                                                          Center: Washington University Genome Sequencing Center code: WUGSC
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This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest.

MAPPING INFORMATION:
Mapping information for this clone was provided by Dr. Wes Warren,
Department of Genetics, Washington University, St. Louis MO. For
additional information about the map position of this sequence, see
http://genome.wustl.edu 8ee

## SOURCE INFORMATION:

brain genomic DNA. The clone and detailed information obtained from Research Genetics, Inc. (http://www.repieter de Jong and coworkers at http://www.chori.org The RPCI-23 BAC Library has been constructed by Kazutoyo Osegawa and Minako Tateno in the laboratory of Pieter de Jong (http://www.chori.org) from female C57BL/6J mouse kidney and/or brain genomic DNA. The clone and detailed information can be obtained from Research Genetics, Inc. (http://www.resgen.com) or

NEIGHBORING SEQUENCE INFORMATION: This sequence is the entire insert overlapped by AC123054. Location/Qualifiers o f the clone.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Match 10.6%;
Local Similarity 48.2%;
nes 145; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                          11033 CATATGCAATACATGAGAATCTAATAAATGTAATTTTCATATCAGCCACCTAAACACTCA 11092
                                                                                                                                                                                                                                                                                                                11093 CAGTTATATTTTAATTCTTGTAATTTTAGTATATGAAAATAATAAATTTTAACTACTTTT
                                                                                                                          11273 C 11273
                                                                                                                                                                                      11213 CCTTCTCAATTTTACCCCTTCCTTCAACCTCTTCCATTTGCCATTACCAGGTTCCATCACA 11272
                                                                                                                                                                                                                                                    11153 TAAATTAATATTTCTGAAAATTTCTGGCATGTGTATTGTATTCACATCACTTTTACCCCT
                                                                                                                                                                                                                                                                                                                                           137 AACTTAATAAATAATATTTCTCTATCTTTAAAGGCACATATTACGTGGCTAAGGCAATT 196
                                                                                                                                                        317 C 317
                                                                                                                                                                                                                                                                                                                                                                                                    77 GATATATGGTTGTGTGTAACTTATTTATTTGAGAGGTATTTTAACACACCCTTAGAACTAA 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     17 AAGTGACTCCTTCGTTGCGTAGACAGTATGAAAATATTTTTACTGTGATACTTACAAGTT
             Homo sapiens chromosome 11, clone RP11-514F3, complete sequence.
AC087277.11
                                             AC087277
                                                                                                                                                                                                                                                                          ACAGCTGATATACTGTAAAACTCATGTCGCCACTAAATTCTTCTAACACGCGTTCTGTCT 256
                                                                                                                                                                                                                   CTTTCCAAGGGACTCCGAATATGCCACTATTTATCTGTGGCATTTCCCAATTTATATTCCC 316
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52274.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /rpt_tamily="] 51765. .51952
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49190. .50095
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48777. .49054
GI:20147901
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1. .52574
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 51.4; DB 9;
Pred. No. 1;
0; Mismatches 156;
                                             196859 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 206926;
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                                             linear PRI 24-APR-2002
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SOURCE ORGANISM ACCESSION VERSION KEYWORDS

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homo sapiens Homo sapiens (human)

REFERENCE AUTHORS TITLE Hominidae; Homo.

1 (bases 1 to 196859)

Birren, B., Linton, L., Nusbaum, C. and Lander, E.
Homo sapiens chromosome 11, clone RP11-514F3 Unpublished

JOURNAL REFERENCE AUTHORS 2 (bases 1 to 196859)

Birren, B., Linton, L., Nusbaum, C., Lander, E., Allen, N., Anderson, S., Barna, N., Bastien, V., Boguslavkiy, L., Boukhgalter, B., Brown, A., Camarata, J., Campopiano, A., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Faro, S., Ferreira, P., Fitchugh, W., Gage, D., Galagan, J., Gardyna, S., Ginde, S., Goyette, M., Graham, L., Grand-Pierre, N., Hagos, B., Heaford, A., Horton, L., Hulme, W., Iliev, I., Johnson, R., Horton, E., Liu, G., Macque, R., Landers, T., Lehoczky, J., Levine, R., Liu, G., MacLean, C., MacGaran, K., Mathews, C., McCarthy, M., McEwan, P., McKernan, K., McPheeters, R., Meldrim, J., Meneus, L., Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Nguyen, C., Norbu, C., Norman, C.H.,

REFERENCE AUTHORS

TITLE JOURNAL

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O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Follara, V., Raymond, C., Retea, R., Risack, R., Risack, R., Reback, R., Rilay, R., Risack, R., Raymond, C., Regov, P., Ramond, J., Rosetti, M., Rilay, R., Risack, R., Raymond, C., Regov, P., Ramond, J., Rosetti, M., Rilay, R., Risack, R., Raymond, C., Raden, S., Sterry, P., Sarylas, R., Ramond, R., Raymond, C., Raden, S., Raymond, C., Raden, R., Ramond, R., Ramond, R., Raden, R., Raden, R., Ramond, R., Raden, R
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TITLE JOURNAL

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   complement (2441. .2542)
/rpt_family="L2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /rpt_family="AluSg"
complement(1696. .2027)
/rpt_family="MLT1F1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone_lib="RPCI-11 Human Male BAC"
complement(1362. .1667)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /rpt_family="L1MC4a"
complement(2895. .32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            complement (3996.
                         /rpt_family="FLAM_A" complement(16491. . . 1
                                                                                                                                                                                                                                                                                                            complement(11082. .11330)
/rpt_family="MIR"
                                                                                                                                                                                                                                                                                                                                                                 complement(9716. .10072)
/rpt_family="L2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      complement (5971. .6301)
/rpt_family="L2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   complement (5756.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ocation/Qualifiers
/rpt_family="L1MC4a"
                                                                                                                                                                                                                                                                                                                                                                                                                                           'rpt_family="AluJb"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     db xref="taxon:9606"
chromosome="11"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ğ
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                                                                                                                                                                                                                                                                                                                                                                                                                  _family="CT-rich"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    family="MLT1A1"
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ement(507
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       family="AT_rich"
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                                                                                                                                                                                                                   family="MLT1C"
. .13679)
                                                                                                                                                                                                                                                           family="MIR"
                                                                                                                                                                                                                                                                                                                          family="MER103"
ement(11077)
                                                                                                                                                                                                                                                                                                                                                                                             family="MIR3"
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                                                                family="AluSx"
                                                                                                                   family="AT_rich"
                                                                                                                                                                                                                                                                                    family="MIR"
                                                                                                                                                              .3852
                                                                                                                                                ly="MER58"
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Park

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RESULT 14
AC124696
                                                                                 KEYWORDS
SOURCE
                                                                                                                                   ACCESSION
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                                                                                                                                                                                                            LOCUS
DEFINITION
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Best Local Similarity 45.3
Matches 185; Conservative
                                                            ORGANISM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     43 TATGAAAATATTTTTACTGTGATACTTACAAGTTGATATATGGTTGTGTGTAACTTATTT
Mus musculus
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
                                                                                                                                                         AC124696 193849 bp DNA linear HTG 29-APR-2005 Mus musculus chromosome 16 clone RP24-173I13, WORKING DRAFT SEQUENCE, 8 unordered pieces.
AC124696
                                                                         HTG; HTGS PHASE1; HTGS_DRAFT; HTGS_ACTIVEFIN.
                                                                                                                                     AC124696.4 GI:62955023
                                                                                                                                                                                                                                                                                                                                                                           CTATTTATCTGTGGCATTTCCAATTTATATTCCCCTATTGGGTATTTGATGTGGCCGTTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TTCAATTTATCTAAAGCAAGTTTTGTATAATTCAAAATACTTTGCTTT 450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /rpt family="MTR"
complement (19648. .19723)
/rpt family="L2"
20222. .2040"
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complement(22225. .22279)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /rpt_family="AluSx"
complement(20797. .:
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20431.
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ement(2222
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ement (17777
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0; Mismatches 223;
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Pred. No. 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       JOURNAL
                                                                               misc_feature
                                                                                                                                                                                 misc_feature
                                                                                                                                                                                                                                                                                                                                                source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequencing vector: M13; 0% sequencing vector: plasmid; 100% sequencing vector: plasmid; 100% Chemistry: Dye-primer ET; 0% of reads Chemistry: Dye-terminator Big Dye; 100% of reads Assembly program: Phrap; version 0.990319 Consensus quality: 191374 bases at least Q40 Consensus quality: 192113 bases at least Q30 Consensus quality: 192485 bases at least Q30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Wilson,R.K.
Direct Submission
Submitted (29-APR-2005) Genome Sequencing Center, 4444 For.
Parkway, St. Louis, MO 63108, USA
On Apr 29, 2005 this sequence version replaced gi:24416033
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (15-JUN-2002) Genome Sequencing Center, 4444 Forest Parkway, St. Louis, MO 63108, USA 3 (bases 1 to 193849)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 (bases 1 to 193849)
McPherson, J.D. and Wat
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The sequence of Mus musculus clone Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Web site:http://genome.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Center: Washington University Genome Center code: WUGSC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Wilson, R.K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Center project name: M_BB0173I13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: submissions@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NOTE: This is a 'working draft' sequence. It currently consists of 8 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1053
1153
2248
2348
3389
3489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4997
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1153. .2247
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                                                                                                                                                           note="assembly_name:Contig23"
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                                                                                                                                                                                                               clone="RP24-173I13"
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                                                                                                                                                                                                                                                                /mol_type="genomic DNA"
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                                                                                                                                                                                                                                                                                                                                                                           ocation.
                                                                                                                                                                                                                                                                                                                    organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       --- Project Information
                                                                                                                                                                                                                                                                                                                                                .193849
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                                                                                                                                                                                                                                                                                                                                                                                                 80358: gap of
193849: contig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Summary Statistics
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                                                                                                                                                                                                                                                                                                                                                                           'Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gap of unknown l
contig of 1508 k
gap of unknown l
contig of 1527 k
gap of unknown l
contig of 2731 k
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            gap of unknown contig of 1095 length of unknown contig of 1041 length of 1041 len
                                                                                                                                                                                                                                                                                                                                                                                                 gap of unknown length
contig of 70704 bp in length
gap of unknown length
contig of 113491 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 bp in length
n length
8 bp in length
n length
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n length
l bp in length
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length
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REFERENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ACCESSION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
Allen, C., Allen, H., Alsbrooks, S., Amin, A., Anguiano, D.,
Anyalebechi, V., Aoyagi, A., Ayodeji, M., Baca, E., Baden, H.,
Baldwin, D., Bandaranaike, D., Barber, M., Barnstead, M., Benahmed, F.,
Biswalo, K., Blair, J., Blankenburg, K., Blyth, P., Brown, M.,
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Cardenas, V., Carter, K., Cavazos, I., Ceasar, H., Center, A.,
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Claveland, C., Cockrell, R., Cox, C., Coyle, M., Cree, A., D'Souza, L.,
Davila, M. L., Davis, C., Davy-Carroll, L., De Anda, C., Dederich, D.,
Delgado, O., Denson, S., Deramo, C., Ding, Y., Dinh, H., Divya, K.,
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Egan, A., Escotto, M., Eugene, C., Evans, C.A., Falls, T., Fan, G.,
Fraser, C.M., Gabisi, A., Ganta, R., Garcia, A., Garner, T., Garza, M.,
Gebregeorgis, E., Geer, K., Gill, R., Grady, M., Guerra, W., Guevara, W.,
Gunaratne, P., Haaland, W., Hamilton, C., Hamilton, K.,
Harvor, V., Hawson, A., Hernander, J., Hamilton, K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       84581
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            84641 ATGTATGTACACATCGCAGATGGAGTTTACAATTTGAGCTGACA 84684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        163
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AC163463.2 GI:68300099
HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_ENRICHED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AC163463 244638 bp
Bos taurus clone CH240-125K20, ***
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   unordered pieces
                                                                                                                                                                                                                                                                                                                                                                                             Muzny, D. Marie., Metzker, M. Lee., Abramzon, S., Adams, C., Alder, J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bos taurus (cow)
                                                                                                                                                                                                                                                                                                                                                                                                                                              Pecora; Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CTTTAAAGGCACATATTACGTGGCTAAGGCAATTACAGCTGATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TATGAAAATATTTTTACTGTGATACTTACAAGTTGATATATGGTTGTGTGTAACTTATTT 102
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80359. .193849
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              note="assembly_name:Contig48"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /estimated_length=unknown
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  estimated_length=unknown
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                estimated
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Pred. No. 1.6;
0; Mismatches 71;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DNA linear HTG 01-JUL-2005
SEQUENCING IN PROGRESS ***, 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 193849;
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JOURNAL
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AUTHORS
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AUTHORS TITLE JOURNAL

COMMENT

Center project name: FHXA
Center clone name: CH240-125K20
Center clone name: CH240-125K20
Center clone name: CH240-125K20
Center Summary Statistics
Assembly program: Atlas 3.0;
Censensus quality: 229556 bases at least Q40
Censensus quality: 239565 bases at least Q30
Censensus quality: 236194 bases at least Q20
Bstimated insert size: 239301; sum-of-centigs estimation
Dstimated insert size: 239301; sum-of-centigs estimation

Quality coverage: 4x in Q20 bases; sum-of-contigs estimation

Center code: BCM

Center: Baylor College of Medicine

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Jackson, L., Jacob, L., Jiang, H., Johnson, B., Johnson, R., Jolivet, A.,
Karpathy, S., Kelly, S., Kally, S., Khan, Z., King, L., Kovar, C.,
Kowis, C., Kraft, C.L., Lebow, H., Levan, J., Lewis, L., Li, Z., Liu, J.,
Liu, J., Liu, W., Liu, Y., London, P., Longacre, S., Lopez, J.,
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Plopper, F., Poindexter, A., Popovic, D., Primus, E., Pu, L.-L.,
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Reilly, B., Reilly, M., Ren, Y., Reuter, M., Richards, S., Shen, H.,
Sanders, W., Savery, G., Scherer, S., Scott, G., Shatsman, S., Shen, H.,
Shetty, J., Shvartsbeyn, A., Sisson, I., Siter, C.D., Smajs, D.,
Shetty, J., Strong, R., Sutton, A., Svatek, A., Tabor, P., Taylor, C.,
Taylor, T., Thomas, N., Thomas, S., Tingey, A., Trejos, Z., Usmani, K.,
Wang, O., Wang, S., Warren, R., Walker, B., Wang, J.,
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Wang, O., Wang, S., Warren, R., Walker, B., Wang, J.,
Wang, O., Wang, S., Warren, R., Walker, B., Wang, J.,
Wang, O., Wang, S., Warren, R., Walker, B., Wang, J.,
Wang, O., Wang, S., Warren, R., Walker, B., Wang, J.,
Wang, O., Wa
                                                                         AL Submitted (01-7UL-2005) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
On Jun 29, 2005 this sequence version replaced gi:67514619.
The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (http://www.hggc.bcm.tmc.edu/projects/rat/). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence only contigs will be indicated in the feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (12-dUN-2005) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA 3 (bases 1 to 244638)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Worley, K.C.
Direct Submission
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-- Genome Center
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NOTE: Estimated insert size may differ from sequence length

(see http://www.hgsc.bcm.tmc.edu/docs/Genbank draft_data.html).

NOTE: This is a "working draft" sequence. It currently

consists of 39 contigs. The true order of the pieces
is not known and their order in this sequence record is
arbitrary. Gaps between the contigs are represented as

runs of N, but the exact sizes of the gaps are unknown.

This record will be updated with the finished sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            as soon as it is available and the accession number will be preserved.
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                                        26098 gap of 50 bp
37514 contig of 11416 bp in length
38190 gap of 676 bp
55334 contig of 17144 bp in length
55384 gap of 60 bp
75854 contig of 20470 bp in length
76343 gap of 489 bp
76344 contig of 20470 bp in length
76394 gap of 50 bp
83875 contig of 7481 bp in length
83925 gap of 50 bp
94134 contig of 10209 bp in length
94267 gap of 133 bp
97784 contig of 10209 bp in length
10258 gap of 50 bp
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115932 gap of 50 bp
115932 gap of 50 bp
121475 contig of 6624 bp in length
131723 gap of 50 bp
131673 contig of 10148 bp in length
140128 gap of 50 bp
140128 gap of 50 bp
140128 gap of 50 bp
181837 contig of 8305 bp in length
151022 gap of 50 bp
181837 contig of 10904 bp in length
151022 contig of 30755 bp in length
151022 contig of 627 bp in length
151023 contig of 6287 bp in length
181847 contig of 6291 bp in length
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                     399 GGTCTTCAATTTATCTAAAGCAAGTTTTGTATAATTCAAAATACTTTGCTTT
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Ado39660 Yeast chi
Abl32718 Human imm
Aas61080 Human gen
Abg66998 Human imm
Abg15253 Oligonucl
Abg15253 Oligonucl
Ac135363 Rice stre
Ad271063 Human chr
Aby99761 Human pfx
Aas46704 Tumour su
Ab132929 Human imm
Ab13292 Chemicall
Ab143362 Human pol
Ab143363 Rice stre
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Aba92787 Buchnera	Abl33023 Human imm	_		Abk28232 DNA trans	Aas45387 Chemicall		Aas46788 Tumour su	Abz10246 Haematopo	Aas61176 Human gen	Adw94163 Staphyloc	Acf75038 Staphyloc	Aaf25334 Nucleotid	Aeb80195 Human tra	Abn83124 Human vol	Adb92131 Human MDR	Adb96940 Human MDR	Adb87957 Human UGT	Adb20868 MRP1 base	Acf62749 Cancer ba	Human	Adb92123 Human MDR	Human	Adb87949 Human UGT	Adb20860 MRP1 base	Acf62745 Cancer ba

## ALIGNMENTS

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RESULT 1
ADO39580
Heterologous gene; expression cassette; gene expression; yeast; CAL1; gene; ds.
                                                                                     Wilkinson JQ,
                                                                                                                                      20-JUN-2003; 2003US-00600230
                                                                                                                                                    13-MAY-2004.
                                                                                                                                                                             Saccharomyces cerevisiae.
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                                                                         WPI; 2004-374960/35.
                                                                                                  (WILK/) WILKINSON J
(MCBR/) MCBRIDE K.
(BERT/) BERTAIN S.
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The present invention relates to heterologous genes comprising non-plant 3'-termination sequences and plant expression cassettes incorporating the heterologus genes. The invention is useful for gene expression in plant cells. The present sequence is yeast CALI 3'-termination DNA. This sequence is used in the invention.

New recombinant expression cassette comprising a promoter that functional in plants, operably linked with a coding sequence an plant 3' termination sequence, useful for gene expression in pl

at is and a plant

noncells.

Claim 4; SEQ ID NO 1; 74pp; English.

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RESULT 2
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Best Local Simi
Matches 485;
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                                                                                                                                                                                                                                                                                                                                                                                        Heterologous gene; chitin synthase 3;
                       Wilkinson JQ,
                                                                                                                                                                                                                                                                                                   US2004092020-A1
                                                                                                                                                                                                                                                                                                                                                Saccharomyces cerevisiae
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Yeast chitin synthase 3 CAL1 gene
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                                                                 (WILK/) WILKINSON J
(MCBR/) MCBRIDE K.
(BERT/) BERTAIN S.
                                                                                                                                                             20-JUN-2002; 2002US-0390529P
                                                                                                                                                                                                          20-JUN-2003; 2003US-00600230
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Pred. No. 3.3e-104;
); Mismatches 0;
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RESULT 3
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Huma
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26-MAR-2002

(first

entry) associated

gene

SEQ ID

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ABL32718 standard;

DNA;

5739

Human; immune system disease; cytosine methylation; antiasthmatic; antiarteriosclerotic; antianaemic; cytostatic; nootropic; neuroprotective; anti-HIV; anticonvulsant; ophthalmological; antirheumatic; antiarthritic; antidiabetic; antipsoriatic; antiarthritic; antidiabetic; antipsoriatic; antiinflammatory; cancer; eye disease; arteriosclerosis; anaemia; acute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy; neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease; ds.

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Best Local Simi
Matches 476;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New recombinant expression cassette comprising a promoter that is functional in plants, operably linked with a coding sequence and a plant 3' termination sequence, useful for gene expression in plant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 4046 BP; 1211 A; 739 C; 819 G; 1277 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure;
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GENBANK; X57300.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                is used in the invention.
              TGTATAATTCAAAATACTTTGCTTTTCTCCATGACTTGAACCTCCAAATGATGAGGTA
                                                                      ACTTGTTCGAGTTTTGCTCTTTTGCTCTAAAGGTCTTCAATTTATCTAAAGCAAGTTT
                                                                                                              TTTATATTCCCCTATTGGGTATTTGATGTGGCCGTTTAAATAGTCACCGATTGAATCTTC
                                                                                                                                                                       GCGTTCTGTCTCTTTCCAAGGGACTCCGAATATGCCACTATTTATCTGTGGCATTTCCAA
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                                                                                                                                                                                                                                                                                                                                              ACTTGTTCGAGTTTTGTCTTTTGCTTCTAAAGGTCTTCAATTTATCTAAAGCAAGTTT
                                                                                                                             TTTATATTCCCCTATTGGGTATTTGATGTGGCCGTTTAAATAGTCACCGATTGAATCTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQ ID NO 81; 74pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         97.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 474.8; DB 12;
Pred. No. 1.2e-101;
0; Mismatches 2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 12;
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RESULT 4
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                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present invention provides a number of human immune system associat genes which are modified by the methylation of cytosines. The sequences can be used in the diagnosis and treatment of immune system disorders, including eye diseases such as retinopathy, neovascular glaucoma and macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid leukaemia, Alzheimer's disease, AIDS, epilepsy, neurofibromatosis, rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel diseases. The present sequence is a gene of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nucleic acid comprising diagnosis and treatment
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01-SEP-2000; 2000DE-01043826
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                                                                                                                                                                              The invention relates to 224 nucleic acid sequences comprising at least CC 18 bases of a chemically pretreated gene associated with gene regulation converte cytosine bases unmethylated at the 5-position to pretreatment converts cytosine bases unmethylated at the 5-position to converte cytosine bases unmethylated at the 5-position to converte cytosine bases unmethylations. The DNA sequences, convenies, to enable analysis of cytosine methylations. The DNA sequences, coligomers (or sets/arrays) and method are useful in the diagnosis of convenies of such diseases) associated with gene regulation and in therapy of such diseases, by enabling analysis of the cytosine methylation patterns of such genes, kits are provided. They are combined in munodeficiency disease, cardiac disorders, haemophilia, solid tumours and cancer, Werner syndrome, asthma, HDR syndrome, Saethre-Chotzen syndrome, renal disease, preeclampsia, graft versus-host disease. The present sequence is a sequence included in the sequence data for this patent did not form part of the consider of the cytosiated specification, but was obtained in electronic format directly in the sequence for the cytosiated constraints.
                                                                 Query Match
Best Local S
Matches 181
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07-APR-2000;
30-JUN-2000;
01-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New nucleic acid sequences from chemically modified genes associated with gene regulation, useful for analyzing cytosine methylations for diagnosis and therapy of diseases e.g. severe combined immunodeficiency disease.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; Gene regulation-associated gene; severe combined immunodeficiency; cardiac damage; inflammatory response; Haemophilia; Werner syndrome; asthma; HDR syndrome; congenital heart defect; Saethre-Chotzen syndrome; renal disease; Preeclampsia; cardiac allograft vascular disease; colorectal cancer; thyroid cancer; oesophageal cancer; ds; tumour; immunostimulant; cardiant; antiinflammatory; coagulant; antiasthmatic; nephrotropic; gynecological; anti-tumour; immunosuppressive; cytostatic.
                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim
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                                                                                                                                                                  ted specification, WIPO at ftp.wino
                                                                  181;
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nilarity 46.8%;
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The invention relates to a nucleic acid (I) comprising a segment of 18 bases of chemically pretreated DNA of anglogenesis-associated genes (II) having sequences (ABQ66971-ABQ67178) or their complements. (I), also related oligomers, are used to evaluate the methylation status and/or single-nucleotide polymorphisms, in anglogenesis-related genes, for diagnosis and treatment of eye diseases, proliferative retinopathy, neovascular glaucoma, solid tumours, inflammation, rheumatoid arthritis, diabetic retinopathy, macular degeneration caused by neovascularisation, psoriasis, arreriosclerosis, inflammatory bowel diseases, ulcers and Crohn's disease. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New nucleic acid fragments from chemically treated angiogenesis-
associated genes, useful for determining methylation status, e.g
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antirheumatic; antiart
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antiarthritic; antidiabetic; antipsoriatic;
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RESULT 6
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Best Local S
Matches 96
                                                                                                                                                                                                                                                                                                                                                                                                                             antiarteriosclerotic; antianaemic; cytostatic; nootropic; neuroprotective; anti-HIV; anticonvulsant; ophthalmological; antirheumatic; antiarthritic; antidiabetic; antipsoriatic; antiinflammatory; cancer; eye disease; arteriosclerosis; ana acute myeloid laukaemia; Alzheimer's disease; AIDS; epilepsy
                                                                                                                                                                                                          01ek
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including eye diseases such as retinopathy, neovascular glaucoma and macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid leukaemia, Alzheimer's disease, AIDS, epilepsy, neurofibromatosis, rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel
                                                 The present invention provides a number of human immune system associa genes which are modified by the methylation of cytosines. The sequence can be used in the diagnosis and treatment of immune system disorders,
                                                                                                                                                                                                                                                            30-JUN-2000; 2000DE-01032529
01-SEP-2000; 2000DE-01043826
                                                                                                                                                                                                                                                                                                                                                                                                                    neurofibromatosis; rheumatoid arthritis; psoriasis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human immune system associated
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                                                                                                      Claim 1; SEQ ID NO 309;
                                                                                                                               methylation
                                                                                                                                           diagnosis and treatment
                                                                                                                                                      Nucleic acid comprising
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               system disease; cytosine methylation;
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                                                                                                                                          fragment of chemically modified gene, useful of diseases associated with abnormal cytosine
                                                                                                    32pp +
                                                                                                                                                                                                          Berlin
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RESULT 7
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This invention describes a novel method for determining the degree of methylation of a particular cytosine in a motif 5'-CpG-3', present in a genomic sample of DNA. The sample is treated chemically to convert cytosine (C) but not methylated C, to uracil, then part of the genomic DNA that contains the target C is amplified to form a labeled amplicon. The amplicon is hybridised to two classes, each with at least one member, of oligonuclectides and/or peptide-nucleic acid (PNA) oligomers and the degree of hybridisation to both classes is determined from the label on the amplicon. From the ratio of labels hybridised to two classes of oligomers, the degree of methylation is calculated. The method is used: (i) for diagnosis and/or prognosis of side effects of therapeutic drugs and of a wide range of diseases, e.g. cancer, disorders of the central nervous, cardiovascular, gastrointestinal and respiratory systems etc., particularly by detecting mutations or single nucleotide polymorphisms
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; cytosine methylation; 5'-CpG-3'; uracil; cytosine; diagnosis; drug; side effect; cancer; central nervous system; cardiovascular; gastrointestinal; respiratory system; single nucleotide polymorphism; SNP; cell differentiation; ds.
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                                                                                                                                                                                                                                                       from chemically treated
                                                                                                                                                                                                                                                                      Determining the degree of cytosine methylation in genomic DNA, useful diagnosis and prognosis, comprises selective hybridization of amplicon
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05-SEP-2000; 2000DE-01044543
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Matches 174
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                                                                                                                                                                                                                                                                                                                                                                                                      Human; cytosine methylation; 5'-CpG-3'; uracil; cytosine; diagnosis; drug; side effect; cancer; central nervous system; cardiovascular; gastrointestinal; respiratory system; single nucleotide polymorphism SNP; cell differentiation; ds.
                                                                                                                                           01-SEP-2000; 2000DE-01043826
05-SEP-2000; 2000DE-01044543
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Oligonucleotide
  WPI; 2002-371829/40
                                               Olek A,
                                                                                                                                                                                                                01-SEP-2001; 2001WO-EP010074.
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                                                                                              EPIGENOMICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AATAGTCACCGATTGAATCTTCACTTGTTTCGAGTTTTTGTCTTTTTGCTTCTAAAGGTCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TATTTATCTGTGGCATTTCCAATTTATATTCCCCTATTGGGTATTTGATGTGGCCGTTTA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATGAAAATATTTTTACTGTGATACTTACAAGTTGATATATGGTTGTGTGTAACTTATTTA 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    517 BP; 356 A; 38 C;
                                                 Piepenbrock
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CGTTTTTTTTTACGTTATTTTTCGTTTAT
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Pred. No. 0.86,
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  methylation of a particular cytosine in a motif 5'-CgG-3', present in a C genomic sample of DNA. The sample is treated chemically to convert cytosine (C) but not methylated C, to uracil, then part of the genomic CC DNA that contains the target C is amplified to form a labeled amplicon. CT The amplicon is hybridised to two classes, each with at least one member, CC of oligonucleotides and/or peptide-nucleic acid (PNA) oligomers and the CC degree of hybridisation to both classes is determined from the label on the amplicon. From the ratio of labels hybridised to the two classes of CC oligomers, the degree of methylation is calculated. The method is used: CC in for diagnosis and/or prognosis of side effects of therapeutic drugs CC and of a wide range of diseases, e.g. cancer, disorders of the central CC nervous, cardiovascular, gastrointestinal and respiratory systems etc., CC particularly by detecting mutations or single nucleotide polymorphisms CC (SNP's); and (ii) for differentiation of cell or tissue types and for C investigating cell differentiation. The method allows the methylation CC investigating cell differentiation. The method allows the methylation CC tatus of many C residues to be determined simultaneously. ABQ13410-CC ABQ54121 represent genomic DNA sequences used to illustrate the method CC disclusion in the degree of cytosine methylation described in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Sim.
Matches 174;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Determining the degree of cytosine methylation in genomic DNA, useful fidiagnosis and prognosis, comprises selective hybridization of amplicons from chemically treated DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 517 BP; 91 A; 32 C; 38 G; 356 T; 0 U; 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       disclosure of the invention
                Rice stress-regulated promoter
                                                       02-JUN-2005
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                                                                                                                                                                                                                                               TCAATTTATCTAAAGCAAGTTTTGTATAAT 433
                                                                                                                                                                                                                                                                                    AATAGTCACCGATTGAATCTTCACTTGTTCGAGTTTTTGCTTTTTGCTTCTCTAAAGGTCT
                                                                                                                                                                                                                                                                                                                                                           TATTTATCTGTGGCATTTCCAATTTATATTCCCCTATTGGGTATTTGATGTGGCCGTTTA
                                                                                                                                                                                                                                                                                                                                                                                                                               CGCCACTAAATTCTTCTAACACGCGTTCTGTCTCTTTCCAAGGGACTCCGAATATGCCAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTTATATTTTTCGTTAATTTTTATTTAGATATTTTATTATTTTTATTTTAATTTTCGTT 122
                                                                                                                           standard; cDNA; 2000
                                                                                                                                                                                                                   CGTTTTTTTTTTACGTTATTTTTCGTTTAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        56pp + Sequence Listing; 56pp; German
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                                                       (first entry)
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                  SEQ ID
                    NO:13926
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    . 86 ;
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Best Local S
Matches 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cells, and plants containing such polynucleotides. Also disclosed are methods for using the polynucleotides and polypeptides to alter the responsiveness of a plant to abiotic stress. The invention is useful in agriculture. The nucleic acid is useful for determining whether a test plant has been exposed to an abiotic stress condition. It is also useful for selecting an agent that alters abiotic stress regulated polynucleotide expression in a plant cell, and to identify a homolog or ortholog to an abiotic stress responsive polynucleotide. The nucleic acid molecule and the polypeptide encoded by it are useful in altering the responsiveness of a plant to an abiotic stress, such as cold stress, salt stress, osmotic stress or any of their combinations. The present sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New stress-responsive nucleic acid, useful responsiveness of a plant, e.g. cereal, to stress, salt stress or osmotic stress.
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26-SEP-2001;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ss; abiotic stress tolerance; transgenic plant; plant; cereal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to novel abiotic stress responsive polynucleotides and polypeptides. Also disclosed are vectors, expression cassettes, host
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2003-248011/24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Kreps J,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      is used in the exemplification of the invention
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73
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2000
                                                                                                                                                                                                                                                                      YYSWAAWKGWWRWSKTTWARRWSWAWRWKTWAKWYRAAYSKWKKKWWYWTRAAWMATRMW
                               ATATTCCCCTATTGGGTATTTGATGTGGCCGTTTAA
                                                                                                 TTCTGTCTCTTTCCAAGGGACTCCGAATATGCCACTATTTATCTGTGGCATTTCCAATTT 308
                                                                                                                                   <u>AKWYWTKYWTWRRAGWMYRYRTMKMTSWCYTWWMRWMWWYWTTTWYRWRKAMRKARGRA</u>
                                                                                                                                                                                                                                   AGAACTAAAACTTAATAAATAATATTTCTCTATCTTTAAAGGCACATATTACGTGGCTA
                                                                                                                                                                                                                                                                                                     TACAAGTTGATATATGGTTGTGTGTAACTTATTTATTTGAGAGGTATTTTAACACACCTT
                                                                                                                                                                                                                                                                                                                                      AAGGAAGTCGTTTAGSWCMWTKTWWWWKTMRMWMKTKKAWAKAWAWAYYMYSMRYRWMY 314
                                                                                                                                                                                                                                                                                                                                                                   AAGGAGGAAAGTGACTCCTTCGTTGCGTAGACAGTATGAAAATATTTTTTACTGTGATACT
MSGSAGYMTKYAKYWMMTRWKTRKTKRTSWKAWWM
                                                                GTMWWWRKYAWSWTWTKKRKWYMWKRTMRYWKYCCKRAWMSWCYTKSWWWWYKMSTWSKR
                                                                                                                                                                 AGGCAATTACAGCTGATATACTGTAAAACTCATGTCGCCACTAAATTCTTCTAACACGCG
                                                                                                                                                                                                     TWMTTWWARKWTRYWWAKWTYAMWWTKYAAWAAWTATWTKWATRGAWWTRWSWAGWMAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Briggs SP, Co.
T, Provart N,
                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
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2001US-0325277P.
2001US-0332132P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BP; 540 A; 344 C; 416 G; 428 T; 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ID NO 13926; 89pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                    9.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cooper B,
                                                                                                                                                                                                                                                                                                                                                                                                      147;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ricke D,
                                                                                                                                                                                                                                                                                                                                                                                                    Score 43.6; DB
Pred. No. 1.7;
47; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             å
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Glazebrook J,
                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             for altering the an abiotic stress such
                                                                                                                                                                                                                                                                                                                                                                                                        146;
                               344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Goff SA,
                                                                                                                                                                                                                                                                                                                                                                                                                                     Length
                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        272 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Katagiri
                                                                                                                                                                                                                                                                                                                                                                                                      0,
                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         acid
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                                                                                                                                                                                                                                      188
                                                                                                                                                                                                     194
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RESULT 10
ACL37108/c
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                                                                                                                                                                                                                                                                  Query Match
Best Local S
Matches 55
                                                                                                                                                                                                                                                                                                        The invention relates to novel abiotic stress responsive polynucleotides and polypeptides. Also disclosed are vectors, expression cassettes, host cells, and plants containing such polynucleotides. Also disclosed are methods for using the polynucleotides and polypeptides to alter the responsiveness of a plant to abiotic stress. The invention is useful in agriculture. The nucleic acid is useful for determining whether a test plant has been exposed to an abiotic stress condition. It is also useful for selecting an agent that alters abiotic stress regulated polynucleotide expression in a plant cell, and to identify a homolog or ortholog to an abiotic stress responsive polynucleotide. The nucleic acid molecule and the polypeptide encoded by it are useful in altering the responsiveness of a plant to an abiotic stress, such as cold stress, salt stress, osmotic stress or any of their combinations. The present sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New stress-responsive nucleic acid, useful responsiveness of a plant, e.g. cereal, to stress, salt stress or osmotic stress.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                22-JUN-2001; 2001US-0300112P.
24-AUG-2001; 2001US-0314662P.
26-SEP-2001; 2001US-035277P.
21-NOV-2001; 2001US-0332132P.
                                                                                                                                                                                                                                                              Sequence 2000 BP; 510 A; 350 C; 268 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 48; SEQ ID NO 15671; 89pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO2003008540-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Oryza sativa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rice stress-regulated promoter SEQ ID NO:15671
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ACL37108 standard; cDNA; 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21-JUN-2002; 2002WO-US019668
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    agriculture.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ss; abiotic stress tolerance; transgenic plant; plant; cereal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     02-JUN-2005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (SYGN ) SYNGENTA PARTICIPATIONS
                                                                                                                                 451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ġ
                                                                                                                                                                                                55;
                                                                                                                                                                 9
                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                               in the exemplification of the invention
                                                                               KGTRRYYYRMKRAAYWTRWMATRSATWCTGWTYWTSAKTTKWKRWAGYAKATTMKMRKTY
                             TTAGAACTAAAACTTAATAAATAATATTTCTCTATCTTAAAAGGCACATATTACGTGGC
                                                                                                                             ARKAWGKARWAYCKRITAYATMITITRRIRAAWWYYTGMRKRRRSMIRWRMISRWITWSW
                                                                                                                                                            AAGGAGGAAAGTGACTCCTTCGTTGCGTAGACAGTATGAAAATATTTTTACTGTGATACT
                                                             YKWYYYWTRRYRASRARTKGKATKYTMTWKWMMGCWSYTKARWWMMAYKKSWKMAWYAWT 332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Briggs SP, Cooper B, G:
T, Provart N, Ricke D,
                                                                                                                                                                                                Conservative 206;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                              8.9%;
                                                                                                                                                                                           Score 43; DB 11; L
Pred. No. 2.3;
6; Mismatches 186;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AG
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D, Zhu T;
                                                                                                                                                                                                                                                           518 T; 0 U; 354 Other;
                                                                                                                                                                                                                              DB 11; Length 2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              for altering the an abiotic stress such as
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                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Katagiri
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Sequence 847 BP; 501 A; 17 C;

10 G; 319

T; 0 U; 0 Other

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                                        The invention relates to a purified and isolated DNA sequence having protein production increasing activity comprising at least one bent DN element, and at least one binding site for a DNA binding protein. The purified and isolated DNA sequence comprising a first and a second isolated matrix attachment region (MAR) nucleotide sequence, which is MAR nucleotide sequence selected from a purified and isolated DNA sequence above, a purified and isolated MAR DNA above, a purified and isolated chysMAR element and/or fragment, a synthetic MAR sequence, a sequence complementary to it, its molecular chimera, or its combination and variants, is useful for increasing protein production activity in euclaryotic host cell. The present sequence represents a human chromoson
                                                                                                                                                                                                                                                                                                                                                                                          Mermod N,
Puttini S;
                                                                                                                                                                                                                                                                          New purified and isolated DNA sequence having protein production increasing activity comprises a bent DNA element and a binding site for DNA binding protein, useful for increasing protein production activity is eukaryotic host cell.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ds; matrix attachment region; MAR; protein production
                                                                                                                                                                                                                                           Disclosure; SEQ ID NO 187; 282pp; English.
                                                                                                                                                                                                                                                                                                                                                           WPI; 2005-333507/34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          24-OCT-2003;
06-FEB-2004;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human chromosome 2 contig DNA SEQ ID NO 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADZ71063
                                                                                                                                                                                                                                                                                                                                                                                                                                           (SELE-) SELEXIS SA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    YAGGRWWYKKWASSRTWKWCWYKMYMWATKKSWWSWATTWAWKSMWYKKKWTYYTYMTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TAAGGCAATTACAGCTGATATACTGTAAAACTCATGTCGCCACTAAATTCTTCTAACACG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MRKTSYYYTKKWWKKMWSSGYYWRYYTTTMS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KRCRTRWKGWTRWKTWKMMWRWYKKRTYRMKKSAKWWYMRSGAYRRRWMRRMAYSRRRSW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CGTTCTGTCTCTTTCCAAGGGACTCCGAATATGCCACT--ATTTATCTGTGGCATTTCCA
                                                                                                                                                                                                                                                                                                                                                                                                         Girod PA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2003US-0513574P.
2004EP-00002722.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
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 PRESENTATION OF THE PROPERTY O
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ABV99761/c
ID ABV99761 standard; DNA; 22617 BP.
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Best Local S
Matches 186
                                                                                                                                                                                                                                                                                                                                                       Human; 6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 2; PFKFB2; cytostatic; antidiabetic; gene therapy; cancer; diabetes; SNP; gene; single nucleotide polymorphism.
                                                                                                                                                                                                                                                                                                                                                                                                                 Human PFKFB2 gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABV99761;
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                                                                                                                                                                SgS
                                                                                                                                                                                                                                                variation
                                                                                                                                                                                                                                                                                        variation
                                                                                                                                                                                                                                                                                                                                 Homo sapiens
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                                                                                                            exon
                           variation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TCGCCACTAAATTCTTCTAACACGCGTTCTGTCTCTTTCCAAGGGACTCCGAATATGCCA 282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CTATTTATCTGTGGCATTTCCAATTTATATTCCCCTATTGGGTATTTGATGTGGCCGTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TTCAATTTATCTAAAGCAAGTTTTGTATAATTCAAAATACTTTGCTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAATAGTCACCGATTGAATCTTCACTTGTTCGAGTTTTGTCTTTTGCTTCTCTAAAGGTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8.7%; ilarity 45.6%; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                            (first
                                                                                                                                                                                                                                                                                        replace (1342,G)
                                                                                                                                                                                                                                             /standard name= "Single nucleotide polymorphism"
replace (1366,T)
                                                                                                                                                                                                                                                                                                       ocation/Qualifiers
              replace(10169,A)
/*tag= g
                                                                                                                                                                                                        /standard_name= "Single
ceplace(1686,A)
/standard_name= "Single nucleotide polymorphism"
                                                                 217. .10307
                                                                                                                                                                *tag= c
standard_name= "Single
132. .20748
                                                                                 number= 1
                                                                                                                           note=
                                                                                                                                        product= "PFKFB2"
                                                                                                                                                                                                                                                                                                                                                                                                                                            entry)
                                                                                                            .3216
                                                                                                                           "Contains 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 42.4; DB 14;
Pred. No. 2.8;
0; Mismatches 221;
                                                                                                                           introns"
                                                                                                                                                                              nucleotide polymorphism'
                                                                                                                                                                                                                        nucleotide
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                                                                                                                                                                                                                        polymorphism'
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/*tag= n
/number-
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/*tag= i
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/*tag= h
  /standard_name= "
18658...18787
/*tag= ae
/number= 11
18788...19565
                                                                                                                                                                                                                                                                                                                                                                 /number= 7
15873. .16080
/*tag= w
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/number= 6
13406. .13530
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/number= 6
12186. .13405
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                                                                                                                                                                                                          /number= 9
17799. .17903
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16686. .17798
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.0976. .11072
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1566. .11702
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gstandard_name= "Single nucleotide polymorphism"
7904.18657
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                                                                                                                                                                                                                                                                                                                                   6081. .16538
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*tag= v
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number= 5
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                                                                                        eplace (17911, A)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            exon
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                                                                                                                                                                                                                                                                                                                New 6-phosphofruoto-2-kinase/fructose-2,6-bisphosphatase 2 (PFKFB2) gene variants, for improving efficiency and reliability in the development of drugs for treating diseases associated with PFKFB2 activity e.g. cancer.
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                                                                                                                                                                                                                                                                                            Example 1; Fig 1; 95pp; English.
                                                                                                                                                                                                                                                                                                                                                                                              Duda A,
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  163
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                                                                                                              l Similarity 77; Conser
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  CTTTAAAGGCACATA 177
                                            TATATAAAGATATATATAAATATATAAAAGATATATAAAAGATATATATAAAATATAT
                        Conservative
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19566
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replace(21098,G)
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/*tag= ak
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/*tag= aj
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                                                                                                             Score 42.2; DB Pred. No. 5.5; 0; Mismatches
                                                                                                              0;
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                                                                                                                                   DB 6;
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43 TATGAAAATATTTTTACTGTGATACTTACAAGTTGATATATGGTTGTGTGTAACTTATTT 102

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Similarity

8.7%;

Conservative

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                                                                                          The invention relates to a nucleic acid comprising a sequence of 18 cc bases, of a segment of chemically pretreated DNA (CP DNA) e.g. with CC bisulphite, of genes associated with tumour suppression and oncogenes CC having a sequence taken from 536 (actually 533 since numbers 408, 458 and CC 500 are missing from the sequence listing) sequences (Ss) and sequences CC complementary to (Ss). The nucleic acid may be a peptide nucleic acid coligomer (PNA) of at least 9 nucleotides and may form part of a set of CC probes for detecting the cytosine methylation state and/or single CC nucleotide polymorphisms and also to be used in an array for analysing CC diseases associated with CpC dinucleotides e.g. cancers and tumours. The probes can also be used in a method for ascertaining genetic and/or cytosine methylations. The parameters may be compared to annalysing CC diseases or the predisposition to specific diseases, by analysing CC diseases or the predisposition to specific diseases, by analysing CC genetic and/or epigenetic parameters may be compared to anather set of CC genetic and/or prognosis events which are disadvantageous to CC patients. The present sequence is one of the 533 genomic sequences CC derived from tumour suppressor genes and oncogenes. Note: The sequence CC data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Fragments of chemically modified genes associated with tumor suppressor genes and oncogenes, useful in designing primers and probes for analyzing diseases associated with cytosine methylation state e.g. cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15-MAR-2000; 2000DE-01013847.
06-APR-2000; 2000DE-01019058.
07-APR-2000; 2000DE-01019173.
30-JUN-2000; 2000DE-01032529.
01-SEP-2000; 2000DE-01043826.
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tumour; CpG dinucleotide; single-nucleotide polymorphism; SNP;
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   Sequence 14615 BP;
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                                                                           ftp.wipo.int/pub/published_pct_sequences
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4072 A; 253 C; 3233 G; 7057 T; 0 U; 0 Other
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RESULT 14
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Matches 173
                                                                                                                                                        The present invention provides a number of human immune system associated genes which are modified by the methylation of cytosines. The sequences can be used in the diagnosis and treatment of immune system disorders, including eye diseases such as retinopathy, neovascular glaucoma and macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid leukaemia, Alzheimer's disease, AIDS, epilepsy, neurofibromatosis, the neurofibromatosis and inflammatory/ulcerative bowel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           neuroprotective; anti-HIV; anticonvulsant; ophthalmological; antirheumatic; antiarthritic; antidiabetic; antipsoriatic; antinflammatory; cancer; eye disease; arteriosclerosis; anaemia; acute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABL33929 standard;
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01-SEP-2000; 2000DE-01043826
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               neurofibromatosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; immune system disease; cytosine methylation; antiasthmatic; antiarteriosclerotic; antianaemic; cytostatic; nootropic;
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                                                                                                                                                                                                                                                                                                                        Nucleic acid comprising diagnosis and treatment
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                                                                                                                Sequence
                                                                                                                                              diseases.
                                                                                                                                                                                                                                                                             Claim 1; SEQ ID NO 1902;
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                                                                       Similarity
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TTTGTAÄATTÄGÄTATTTAATAÄGGGTTTÄGTATTTAGAÄTTTÄTAATAATATTTTTAG
                         Piepenbrock
                                                                                                                                            The present sequence is a gene of the invention
                                                         Conservative
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                                                                                                                2041 A; 163 C; 1563 G;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             nemia; Alzheimer's disease; AIDS; epilepsy;
rheumatoid arthritis; psoriasis; bowel dis
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                                                                                                                                                                                                                                                                                                                      fragment of chemically modified gene, of diseases associated with abnormal
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                                                      Score 41.6; DE Pred. No. 6.1; 0; Mismatches
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RESULT 15
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L4; pMS2L5; pMS2L6; MGMT; MSH2; MUDT1; TDG INPPLI; RFC4; DDIT
XRCCG; ataxia telangiettasia; aging; Bloom's syndrome; Cockayn
Nijmegen breakage syndrome; Werner syndrome; immunodeficiency;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-JUL-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABL92291
                                                                                                        New nucleic acid derived from genes associated with DNA repair, for diagnosis, e.g. of ataxia telangiectasia, by determination cytosine methylation.
                                                                                                                                                                            Olek A,
                                                                                                                                                                                                                       30-JUN-2000;
01-SEP-2000;
                                                                                                                                                                                                                                             06-APR-2000;
07-APR-2000;
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                                                                                                                                                                                                                                                                                                                                               Unidentified.
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                                                                                      Claim 1;
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                                                                                      SEQ ID NO 100;
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                                                                                                                                                                            Piepenbrock C,
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2000DE-01019173.
2000DE-01032529.
2000DE-01043826.
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DDIT1L; FANCB;
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acids comprising at least 18 base pairs of the chemically of genes associated with DNA repair selected from PMS2L1, PMS2L2, PMS2L3, PMS2L4, PMS2L5, PMS2L6, MGMT, MS8H2, NUDIRFC4, DDITIL, FANCB, or XRCC8. Nucleic acids of the invent

acids of the invention and related

NUDT1,

INPPL1,

PMS2L12,

The invention relates to nucleic acids containing a sequence of at least 18 nucleotides of chemically treated DNA of genes associated with DNA repair, and their complements. The invention also relates to nucleic acids comprising at least 18 base pairs of the chemically pretreated DNA

Query Match 8.6%; Score 41.6; DB 6; Length 6801; Best Local Similarity 44.1%; Pred. No. 6.1; Matches 173; Conservative 0; Mismatches 219; Indels 0; oligomers, are useful for diagnosis of diseases associated with gene repair, specifically ataxia telangiectasia, aging, Bloom's syndrome, Cockayne syndrome, Nijmegen breakage syndrome or Werner syndrome, immunodeficiency, trichthiodystrophy, Fanconi's anaemia, solid tumours and cancer, particularly by determining status of cytosine methylation and/or by detecting single-nucleotide polymorphisms. Determination of individual methylation patterns may allow development of individualised therapies. The sequences given in records ABL92192-ABL92335 represent chemically pre-treated DNA fragments from genes associated with DNA repair, and their complements. Note: The sequence data for this patent is not represented in the specification, but is based on sequence information supplied by the European Patent Office Sequence 6801 BP; 2041 A; 163 C; 1563 G; 3034 T; 0 U; 0 Other; 5658 TTTTTTTTTTTTCGGTTTCGTTTTTTTATTTTTATTTTGGTTTTTAATTTTAATTT 5717 5478 TCGAAGACGATGTATTGATCGTTAATAAATATATGAAAATATATTATTATTATTACTTATTA 5537 5418 TTTAATAATAGAAAGATAATTTAAATTTAAAAATGAGTAAGGGATTTAAATTGATATTTTT 5477 420 AAGTITTGTATAATTCAAAATACTTTGCTTTT 451 360 ATCTTCACTTGTTCGAGTTTTGTCTTTTTGCTTCTCTAAAGGTCTTCAATTTATCTAAAGC 419 300 TTCCAATTTATATTCCCCTATTGGGTATTTGATGTGGCCGTTTAAATAGTCACCGATTGA 359 240 TAACACGCGTTCTGTCTCTTTCCAAGGGACTCCGAATATGCCACTATTTATCTGTGGCAT 180 ACGTGGCTAAGGCAATTACAGCTGATATACTGTAAAACTCATGTCGCCACTAAATTCTTC 239 120 ACACACCTTAGAACTAAAACTTAATAAATAATATTTCTCTATCTTTAAAGGCACATATT 179 Gaps 299

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Search completed: December 28, 2005, 09:24:31 Job time : 499 secs

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CL104745 ISB1-43I1
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AL09859 Drosophil
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BI815751 PfESToaa3 BH700251 BOMEN12TF	AQ203034 RPCI11-63	AL106008 Drosophi	CC215864 CH261-117	CL486692 SAIL_440	AL620870 T7 end of	BH183920 024_K_20-	CL508886 SAIL_804	AL514901 AL514901	AL100303 Drosophi	AQ451200 HS_5178_A	BM535026 EST588048	AL063932 Drosophil	DN782797 92300960	AL104456 Drosophi	AG552152 Mus muscu	BI814443 PfESToaa2	CD388381 AGENCOURT	AL099601 Drosophi	CE692306 tigr-gss	CD441919 EL01N0402	AL071865 Drosophil

ALIGNMENTS

OY 195 TTACAGCTGATATACTGTAAAACTCATGTCGCCACTAAATTCTTCTAACACGCGTTCTGT	Query Match 13.8%; Score 66.8; DB 9; Best Local Similarity 56.5%; Pred. No. 7.1e-05; Matches 166; Conservative 0; Mismatches 122	ORIGIN	/clone lib="Kluyveromyces delphensis Library"	/clone="KD1625"	/strain="CBS 2170"	/organism="winyveromyces /mol type="genomic DNA"	source 1495	FEATURES Location/Qualifiers	Class: plasmid ends.	Email: swong@tcd.ie	Fax: 353 1 6798558	Tel: 353 1 6082319	Dublin 2, Ireland	Department of Genetics, Smurfit	COMMENT Contact: Wong S	JOURNAL Genome Biol. 4 (2), R10 (2003)		AUTHORS Woug, s., rates, m.A., atmmetmann, m., butler, s. and		Saccharomycetales;	Eukaryota; Fungi;	MSIN	SOURCE Kluyveromyces delphensis	s GSS.	ACCESSION BZ302050	semience.	DEFINITION KD1625.pl Kluyveromyces delphensis Random Genomic Library	
ACTCATGTCGCCACTAAATTCTTCTAACACGCGTTCTGT 254	DB 9; Length 495; 7.1e-05; Nes 122; Indels 6; Gaps 2;		e delphensis Random Genomic			der briefing in						•		Institute		mara Stantaca	1	s for a complete sexual cycle in	j L	Saccharomycetaceae; Kluyveromyces.	charomycotina; Saccharomycetes;					Cross surrous, gonomes carries	s Random Genomic Library	DNA linear GSS 31-OCT-2002

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  111 GGTATTITAACACACCTTAGAACTTAAAACTTAATAAATATATTTCTCTATCTTTAAAG 170
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Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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AL062781
AL062781.1 GI:4943971
GSS.
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/clone_lib="RPCI-98"
/note="end : T7"
                                                                                                                                                                                                                                                                                                                                                   db_xref="taxon:7227"
                                                                                                                                                                                                                                                                                                                                                                                              organism="Drosophila melanogaster"
                                                                                                                                                                                   11.5%;
                                                                                                                                                                                                                                                                                                                                                                      _type="genomic DNA"
                                                                                                                                                                42; Mismatches
                                                                                                                                                                                   Score 55.6; DB Pred. No. 0.027;
<del>=</del>
                                                                                                                                                                                                           DB 10;
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                                                                                                                                                                                                        Length 1001;
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Best Local Similarity 15.6
Matches 62; Conservative
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Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
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BACR08K10 of RPCI-98 library from
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/db_xref="taxon:7227"
/clone="shaCRO8K10"
/clone lib="RPCI-98"
/note="end: TET3"
                                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                                                                           organism="Drosophila melanogaster"
/mol_type="genomic DNA"
                     10.7%; Score 51.8; D
15.6%; Pred. No. 0.2;
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survey sequence TET3 end of BAC #
rom Drosophila melanogaster (fruit
                                               DB 10;
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Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC ilbrary was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; cn bw sp, the same strain used for the BDGP's Pl and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Drosophila melanogaster
Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     fly), genomic survey sequence.
AL069706
AL069706.1 GI:4949849
GSS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Drosophila melanogaster (fruit fly)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAATAGTCACCGATTGAATCTTCACTTGTTCGAGTTTTTGTCTTTTGCTTCTCTAAAGGTC
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                                                                                                                                                                                                                 Location/Qualifiers
                         /clone lib="RPCI-98"
/note="end : T7"
                                                                                                                              organism="Drosophila melanogaster"
|mol_type="genomic DNA"
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   738 TTTATTWT 731
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    446 GCTTTTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         386 TIGCTICTCTAAAGGTCTTCAATTTATCTAAAGCAAGTTTTGTATAATTCAAAATACTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             86 TTGTGTGTAACTTATTTGTTGAGAGGTATTTTAACACACCTTAGAACTAAAACTTAATA 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Xenopodinae; Xenopus; Silurana.

1 (bases 1 to 1191)

Kremitzki, C., Carter, J., McPherson, J., Warren, W., Mardis, E. and Wilson, R.

A physical map of the xenopus tropicalis genome Unpublished (2003)
                                                                                                                                                                                                                                                                                                 High quality sequence start: 36
High quality sequence stop: 397
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                             Email: submissions@watson.wustl.edu
Insert Length: 75000 Std Error: 0.
Seq primer: T7 TAATACGACTCACTATAGGG
Class: BAC ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Genome Sequencing Center
Washington University School of Medicine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ISB1-43I12_T7.1 ISB1 Xenopus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Xenopus tropicalis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CL104745.1 GI:40598380
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Richard K Wilson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Xenopus tropicalis (western clawed frog)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        |- || || |- |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || 
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                                                                                                                                                              /organism="Xenopus tropicalis"
/mol_type="genomic DNA"
/db_xref="taxon:8364"
                                /clone_lib="ISB1"
/note="Vector: pBeloBAC11;
Library Segment 1"
                                                                                                                                     clone="ISB1-43I12"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     bp DNA linear GSS 05-JAN-2004 tropicalis genomic clone ISB1-43I12,
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                                                                    ISB-1 Xenopus tropicalis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         184;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
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Query Match Best Local Similarity

9.9%;

Score 47.8; DB Pred. No. 1.6;

10;

Length

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RESULT 6
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BH945927.1
GSS.
                                                                                                                                                                                                                                                                                                                                                              Brassica oleracea
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids_II; Brassicales; Brassicaceae; Brassica.
                                                                                                                                                                                                                                                                                              Whole genome shotgun reads from Brassica oleracea Unpublished (2002)
Contact: Richard K. Wilson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BH945927 7
obu88a02.b1 B.oleracea002
                                                                                                                                                                                                                   Seq primer: -21UPpOT forward Class: shotgun
                                                                                                                                                                                                                                             Email: submissions@watson.wustl.edu Plate: obu88 row: a column: 02
                                                                                                                                                                                                                                                                      Genome Sequencing Center
Washington University School of Medicine
                                                                                                                                                                                                                                                                                                                                      Delehaunty,K., Fewell,G., Fulton,L., McCombie,W.R., Nash,W., Rabinowicz,P.D. and Wilson,R.K.
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                                                                                                                                                                                         quality sequence start: 26 quality sequence stop: 551
                                /note=TVector: pOTw13; Whole genome shotgun library from flowering buds. DNA was purified from a crude nuclear prep using Brassica oleracea TOI00DHB buds provided by Thosmas Osborn at the University of Wisconsin. Genomic DNA was provided by Pablo Rabinowicz (CSHL) and the shotgun library prepared at Washington University Genome
                     sequencing Center."
                                                                                                                          /mol_type="genomic DNA"
/db_xref="taxon:3712"
                                                                                                                                                                             ocation/Qualifiers
                                                                                                                                                     organism="Brassica oleracea"
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Local Similarity
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Determination of this BAC-end sequence was carried out as part of a Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP) this://www.edgp.ebi.ac.uk - This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CNS0106X 1101 bp DNA LINEAR CONSOLORANT TO THE CONSOLORATION TO THE CONSOLORANT TO THE CO
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AL098595
AL098595.1 GI:5610206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
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/clone_lib="DrosBAC"
/plasmid="pBeloBAC11"
                                                                                                                                                            /mol_type="genomic DNA"
/db_xref="taxon:7227"
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9.7%;

Score 47;

DB 10;

Length 1101;

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RESULT 8
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                                                                                                                                                                                 Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk - This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector
                                                                                                                                                                                                                                                                                                                                                                                          CNS016LI 1101 bp DNA linear GSS 26-JUL-1999 Drosophila melanogaster genome survey sequence T7 end of BAC BACN16D22 of DrosBAC library from Drosophila melanogaster (fruit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AL106896
AL106896.1 GI:5624374
                                                                                                                                                                                                                                                                                                                               Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
                                                                                                                                                                                                                                                                                                                                                                                         Genoscope.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Drosophila melanogaster (fruit fly)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      fly), genomic survey sequence.
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                                                                                                                                                                                                                                                                                                            : www.genoscope.cns.fr)
/clone lib="DrosBAC"
/plasmId="pBeloBAC11"
/note="end : T7"
                                                                        /organism="Drosophila melanogaster"
/mol_type="genomic DNA"
/db_xref="taxon:7227"
                                                                                                                                            Location/Qualifiers
                                                         /clone="BACN16D22"
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2; Mismatches 171;
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Best Local Similarity
Matches 103; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            233 ATTCTTCTAACACGCGTTCTGTCTCTTTCCAAGGGACTCCGAATATGCCACTATTTATCT
                                                                                                                                                                                                                     - Web: www.genoscope.cns.fr)

Determination of this BAC-end sequence was carried out as part of a collaboration with the Suropean Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk -. This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygo
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                            Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fl
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BACN37D10 of DrosBAC library from
                                                                                                                                                                                                                                                                                                                                                                                                                                       Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Drosophila melanogaster (fruit fly)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 genomic survey sequence.
                 /plasmid="pBeloBAC11"
/note="end : SP6"
                                                                           /mol_type="genomic_DN/db_xref="taxon:7227"
/clone="BACN37D10"
                                                                                                                                        organism="Drosophila
                                                                                                                                                                                   Location/Qualifiers
                                                          clone_lib="DrosBAC"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GI:5629115
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31.0%; Pred. No. 2
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Matches Query Match Best Local S

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h 9.5%; Score 46.2; Similarity 14.7%; Pred. No. 3 53; Conservative 170; Mismatch

Mismatches

138; 10;

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The genome of the host-cell transforming parasite Theileria annulate and a comparison with T. parva
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EST.
                                                                                                                                                                                                                            The Wellcome Library: Wilted Kingbom
Genome Campus, CB10 1SA, UNITED KINGBOM
Merozoite cDNA library: Frank Katzer and Brian Shiels, Division of
Merozoite cDNA library: Frank Katzer and University of Glasgow, UK.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AJ929051 Theileria annulata merozoite Theileria annulata cDNA clone tamo230_q1k, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                       Unpublished (2005)
Contact: Pain A
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1 (bases 1 to 1161)
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Location/Qualifiers
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/clone="tam024c03_q1k"
/dev gtage="merozoite"
/lab_host="Bos taurus (cow)"
/clone 11b="Theileria annulata merozoite"
/note="country: Turkey:Ankara"
                                                                                                          /isoTate="Ankara (clone D7)"
/db_xref="taxon:5874"
                                                                                                                                                                          organism="Theileria annulata"
                                                                                                                                                      type="mRNA"
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                                                                                                  ACCGATTGAATCTTCACTTGTTCGAGTTTTGTCTTTTGCTTCTCTAAAGGTCTTCAATTT 410
                                                                                                                                                                      CTGTGGCATTTCCAATTTATATTCCCCCTATTGGGTATTTGATGTGGCCGTTTAAATAGTC 350
                                                                                                                                                                                                          TNATTTATTAATAAGTTATTTACATTAATTTATTTTAGNNTNGTTTTATATAATTTGA
                                                                                                                                                                                                                                                                              GCACATATTACGTGGCTAAGGCAATTACAGCTGATATACTGTAAAACTCATGTCGCCACT
                                                                                                                                                                                                                                                                                                                                                 GATTATNTTATATANTTAÄAANTTAÄÄATTANNTTNNTTTÄTNATTTTTTATNTNNNTAA 875
ATTAATAATGNGATAAAATGAAATGTTAANATTTTATTTT 1153
                                                                                                                                       GTAAG--ATTTTTTTTTTTTTTTTNICNTCCNTGGTTAATTATTTTTTTTTTTTAATATTTTT 1053
                               ATCTAAAGCAAGTTTTGTATAATTCAAAATACTTTGCTTT
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                                                                                                                                                                                                              995
                                                                                                                                                                                                                                                                                                                  230
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SOURCE ORGANISM VERSION KEYWORDS REFERENCE DEFINITION FEATURES ACCESSION JOURNAL TITLE AUTHORS source Pain, A., Renauld, H., Berriman, M., Murphy, L., Yeats, C.A., Weir, W., Kerhornou, A., Aslett, M., Bishop, R., Bouchier, C., Cochet, M., Coulson, R.M. R., Cronnin, A., de Villiers, E., Fraser, A., Fosker, N., Gardner, M., Goble, A., Griffiths-Jones, S., Harris, D.E., Katzer, F., Larke, N., Lord, A., Maser, P., McRellar, S., Mooney, P., Morton, F., Nene, V., O'Neil, S., Price, C., Quail, M.A., Rabbinowitsch, E., Rawlings, N.D., Rutter, S., Saunders, D., Seeger, K., Shah, T., Squares, R., Squares, S., Tivey, A., Walker, A.R., Woodward, J., Dobbelaere, D.A.E., Langsley, G., Rajandream, M.-A., McKeever, D., Shiels, B., Tait, A., Barrell, B. and Hall, N.

The genome of the host-cell transforming parasite Theileria annulata and a comparison with T. parva

Lu Unpublished (2005)

Contact: Pain A The Mellcome Trust Sanger Institute
The Wellcome Trust Sanger Institute
The Wellcome Trust Sanger Institute
The Mellcome Campus, CB10 18A, UNITED KINGDOM
Merozoite CDNA library: Frank Katzer and Brian Shiels, Division
Merozoite CDNA intram and Immunity, ICM, University of Glasgow, Theileria annulata Theileria annulata AJ928310 Theileria annulata merozoite tam017g02\_q1k, mRNA sequence Theileria Eukaryota; Alveolata; Veterinary Infection and Immunity, ICM, Location/Qualifiers (bases 1 to 1079) /mol\_type="mRNA" /isolate="Ankara (clone D7)" organism="Theileria annulata" GI:67498696 Apicomplexa; Piroplasmida; Theileriidae; mRNA linea linear annulata EST 10-JUN-2005 lata cDNA clone Division

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JOURNAL COMMENT
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AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      51 TATTTTTACTGTGATACTTACAAGTTGATATATGGTTGTGTGTAACTTATTTTTTGAGA 110
                                                                                                                                                                                                                                                                                                                                                                                               DU000686 1014 bp DNA linear GSS 323624 Tomato MboI BAC Library Lycopersicon esculentum clone SL MboI0047002'3, genomic survey sequence. DU000686 DU000686.1 GI:72352331 GSS.
                                                                                                                                                                                                                  BAC end sequencing from three Unpublished (2005) Other_GSSs: 241792
                                                                                                                                                      Contact: Lukas Mueller
Tanksley Lab, Dept. of Plant
Cornell University
251 Emerson Hall, Ithaca, NY
                                                                                                                                                                                                                                                                                                                  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; asterids; lamilds; Solanales; Solanaceae; Solanum; Lycopersicon.
                                                                                                                                                                                                                                                                                                                                                               Lycopersicon esculentum
                                                            Seq primer: SP6
Class: BAC ends
                                                                                        Email: sgn-feedback@sgn.cornell.edu Plate: 47 row: O column: 2
                                                                                                                                                                                                                                                                                  Mueller, L.A., Buels, R.M., Wang, Y., Tanksley, S.D., Giovannoni, J.J
                                                                                                                                                                                                                                                                                                                                                                                 Lycopersicon esculentum (Solanum lycopersicum)
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                                                                                                                                                                                                                                                                      Eck, J. and Stack, S.
        quality sequence start: 31 quality sequence stop: 283 Location/Qualifiers
                                                                                                                        607-255-6557
607-255-6683
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone="tam017g02_qlk"
/dev stage="merozolte"
/lab_host="Bos taurus (cow)"
/clone lib="Theileria annulata
/note="country: Turkey:Ankara"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9.4%;
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Pred. No. 4.7;
0; Mismatches 231;
                                                                                                                                                        14853, USA
                                                                                                                                                                                      Breeding
                                                                                                                                                                                                                                                    Solanum lycopersicon libraries
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RESULT 13
CX173493
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AUTHORS
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KEYWORDS
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Best Local
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                                                                                                                                                                                        JOURNAL
                                                                                                                                                                                                                           TITLE
                                                                                                                                                                                                                                                                                                                                                  ORGANISM
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                                                                                                                                                                                                                                                                                                                                                                                                                                  CX173493 698 bp mRNA linear EST:
A09_69-22_01.abl leaf inoculated with Marssonia pathogen
deltiides Populus deltoides cDNA, mRNA sequence.
                                                                Nanjing Forestry University
Longpan road 9#, Nanjing, Jiangsu,
Tel: 086-025-85427412
Fax: 086-025-85427412
                                                                                                                                                                                      Leaf of poplar 
Unpublished (2004)
                                                                                                                                                                                                                                        1 (bases 1 to 698)
Huang, M., Zhang, X., Zhuge, Q.,
Zhang, B. and Wang, M.
                                                                                                                                                                                                                                                                                           Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids I; Malpighiales; Salicaceae; Saliceae; Populus.
                                                                                                                                                    Contact: Minren Huang
Key Laboratory Tree Genetic
                                                                                                                                                                                                                                                                                                                                                  Populus deltoides
                                                                                                                                                                                                                                                                                                                                                                                                       CX173493.1
                                                                                                                                                                                                                                                                                                                                                                  Populus deltoides
                                                 Email: mrhuang@njfu.edu.
                                  POLYA=Yes.
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Location/Qualifiers
1. .698
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|mol type="genomic DNA"
|cultivar="Heinz 1706"
|db_xref="taxon:4081"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone="SL MboI0047002"
/lab_host="B. coli"
/lab_nost="Tomato MboI BAC Library"
/note="Vector: pBeloBAC11; Site_1: MboI"
                                                                                                                                                                                                                                                                                                                                                                                                       GI:56820917
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Saliceae; Populus.
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source

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RESULT 14
CE216145
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AUTHORS
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                                                                                                                                                        The Institute for Genomic Research Department of Eukaryotic Genomics, Rockville, MD 20850, USA
                                                                                                                                                                                                                                                                                                  kırkness,E.F., Bafna,V., Halpern,A.L., Levy,S., Remington,K.,
Rusch,D.B., Delcher,A.L., Pop,M., Wang,W., Fraser,C.M. and
Venter,J.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CE216145 718 bp DNA linear GSS a tigr-gss-dog-17000373053119 Dog Library Canis familiaris
                                                                                                                                                                                                                                                           The dog genome: survey sequencing and comparative analysis Science 301 (5641), 1898-1903 (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                          Canis familiaris
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CE216145.1 GI:35371814
GSS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      genomic survey sequence.
CE216145
                                                                                                                                                                                                                          Contact: Kirkness EF
                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Canis familiaris (dog)
                                                                                                  Email: ekirknes@tigr.org
                                                                                                                                                                                                                                             14512627
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                                                                                                                         301-838-0208
                                                                                                                                            301-838-0200
                                                                                    shotgun.
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/mol type="mRNA"
/mol type="mRNA"
/db_xref="texon:3696"
/clone lib="leaf inoculated with Marssonia pathogen
Populus deltoides"
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/organism="Canis familiaris"
/mol_type="genomic DNA"
                                                               Location/Qualifiers
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Pred. No. 6.4;
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REFERENCE
AUTHORS
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VERSION
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Carninci, P., Shibata, K., Ozawa, Y., Konno, H., Itoh, M., Aizawa, i Carninci, P., Shibata, J., Fukuda, S., Fukunishi, Y., Funayama, T., Akahira, S., Akiyama, J., Fukuda, S., Fukunishi, Y., Funayama, T., Hara, A., Hayatsu, N., Hori, F., Ishikawa, T., Itoh, M., Izawa, M., Hara, A., Hayatsu, N., Kojima, Y., Matsuyama, T., Niitsuma, H., Ocowa, C., Sato, K., Shibata, Y., Shigemoto, Y., Shiraki, T., Sogabe, Owa, C., Sato, K., Shibata, Y., Shigemoto, Y., Shiraki, T., Sogabe,
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AV112242 Mus musculus C57BL/6J 10-day embryo
clone 2610010G18, mRNA sequence.
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Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                       Email: genome-res@rtc.riken.go.jp
Thermostabilization and thermoactivation of thermolabile enzymes l
Thermostabilization and thermoactivation of the synthesis of full length cDI
trehalose and ite application for the synthesis of full length cDI
(Proc. Natl. Acad. Sci. U.S.A. 95(2):520-524 (1998))
Transcriptional sequencing: A method for DNA sequencing using RNA
polymerase (Proc. Natl. Acad. Sci. U.S.A. 95(7):3455-3460 (1998))
Please visit our web site (http://genome.rtc.riken.go.jp) for
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Unpublished (1999)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tel: 81-298-36-9145
Fax: 81-298-36-9098
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Genome Science Laboratory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Chie Owa
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/db_xref="taxon:9615"
/clone_lib="Dog Library"
/note="Site_1: BstXI; Libraries
peripheral blood"
               /dev_stage="10-day embryo"
/clone_lib="Mus musculus C
                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                        strain="C57BL/6J"
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/cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
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	Sequence 13360, A	Sequence 11896, A	Sequence 651, App	Sequence 651, App	•	Sequence 592, App	Sequence 23, Appl	Sequence 15302, A	Sequence 22, Appl	Sequence 80944, A	Sequence 15890, A	Sequence 16336, A	Sequence 12414, A	Sequence 1, Appli	Sequence 1, Appli	Sequence 14083, A	Sequence 4, Appli	Sequence 17763, A	Sequence 2481, Ap	Sequence 13404, A	Sequence 13125, A

ALIGNMENTS

## RESULT 1 US-09-49-016-15296/c Sequence 15296, Application US/09949016 Patent NO. 6812339 Patent NO. 6812339 FAMORIANI: VENTER, J. Craig et al. TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF PILE REFERENCE: CL001307 CURRENT APPLICATION UNUMBER: US/09/949,016 CURRENT FILING DATE: 2000-04-14 ; ORGANISM: Human US-09-949-016-15296 NUMBER OF SEQ ID NOS: 207012 SOFTWARE: FASTSEQ for Windows Version SEQ ID NO 15296 LENGTH: 23669 TYPE: DNA Query Match Best Local & Matches PRIOR APPLICATION NUMBER: 60/241,755 PRIOR FILING DATE: 2000-10-20 PRIOR APPLICATION NUMBER: 60/237,768 PRIOR FILING DATE: 2000-10-03 PRIOR APPLICATION NUMBER: 60/231,498 PRIOR FILING DATE: 2000-09-08 Match 9.0%; Local Similarity 57.8%; 8086 9688 ATATATAGATATATA 9674 163 43 TATGAAAATATTTTTACTGTGATACTTACAAGTTGATATATGGTTGTGTGTAACTTATTT 78; CTTTAAAGGCACATA 177 TATATAAGATATATAAAGATATATAAAGATATATAAAGATATATATAAAATATAT Conservative 0; Score 43.8; DB Pred. No. 0.14; O; Mismatches DB 3; 57; Length 23669; Indels 0; Gaps 102 9689 9749

RESULT 2 US-09-049-016-12575/c ; Sequence 12575, Application US/09949016 ; Patent No. 6812339 ; GENERAL INFORMATION:

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SEQ ID NO 12575

LENGTH: 23672

TYPE: DNA

RCANISM: Human

US-09-949-016-12575
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CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR FILING DATE: 2000-10-20

PRIOR APPLICATION NUMBER: 60/237,768

PRIOR APPLICATION NUMBER: 60/237,768

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR FILING DATE: 2000-09-08

PRIOR FILING DATE: 2000-09-08

PRIOR FILING DATE: 2000-09-08
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CURRENT APPLICATION NUMBER: US/99/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR PILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
PRIOR FILING DATE: 2000-09-08
                                                                                                                                                                                                                                                                     ; ORGANISM: Human
US-09-949-016-14941
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 14941, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
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Best Local :
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SEQ ID NO 14941
LENGTH: 23672
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TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQ ID NOS: 207012
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                                                                                                                                                                            y Match 9.0%;
Local Similarity 57.8%;
hes 78; Conservative
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                                            103
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                                                                                         TATATAAAGATATATAAAAGATATATAAAGATATATAAAAGATATATATAAAAATATAT 9749
                                            ATTTGAGAGGTATTTTAACACACCTTAGAACTAAAACTTAATAATAATAATATTTCTCTAT 162
  Conservative
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                                                                                                                                                                                0;
                                                                                                                                                                                Score 43.8; DB 3;
Pred. No. 0.14;
0; Mismatches 57;
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; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 235..399
US-09-621-976-2813
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US-09-270-767-29720
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                                                                                                                     ; TYPE: DNA
; ORGANISM: Drosophila melanogaster
US-09-270-767-29720
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SOFTWARE: Patent.pm
SEQ ID NO 2813
LENGTH: 832
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GENERAL INFORMATION:
                                                                                                                                                                                              CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 29720
                                                                                                                                                                                                                                                                          PATENT NO. 6703491
GENERAL INFORMATION:
APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
FILE REFERENCE: File Reference: 7326-094
CURRENT APPLICATION NUMBER: US/09/270,767
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Best Local (
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FILE REFERENCE: GENSET.054PR2
CURRENT APPLICATION NUMBER: US/09/621,976
CURRENT FILING DATE: 2000-07-21
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                                         Matches 110;
                                                       Query Match 8.6%;
Best Local Similarity 49.1%;
                                                                                                                                                                             ENGTH: 1358
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                252 TGTCTCTTTCCAAGGGACTCCGAATATGCCACTATTTATCTGTGGCATTTCCAATTTATA 311
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175 ATATTACGTGGCTAAGGCAATTACAGCTGATATACTGTAAAACTCATGTCGCCACTAAAT 234
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                                           Conservative
                                           0; Mismatches
                                                              Score 41.6; DB Pred. No. 0.28;
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                                                                                Length 1358;
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RESULT 6
US-09-270-767-13702
; Sequence 13702, Application US/09270767
; Patent No. 6703491
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APPLICANT: Homburger et al.
APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
FILE REFERENCE: File Reference: 7326-094
CURRENT APPLICATION NUMBER: US/09/270,767
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 13702
LENGTH: 267
                                                                                                                                                                                                    Patent No. 5670367
GENERAL INFORMATION:
APPLICANT: DORNER,
                                                                                                                                                                                                                                      Sequence 14, Appli
Patent No. 5670367
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Best Local (
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                                                                                                              APPLICANT: SCHEIFLINGER, F.
APPLICANT: FALKUER, F. G.
TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
COMPUTER READABLE FORM:
                                                                                ADDRESSEE:
STREET: 18
                            COUNTRY:
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110; Conserv
                                                                   Alexandria
                   22313-0299
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                                                                                  1800 Diagonal Road,
                                 USA
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                                                                                                                                                                                                        DORNER, F.
                                                                                                  Foley & Lardner
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                                                                                    Suite
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US-10-030-808-1

Sequence 1, Application US/10030808 Patent No. 6887677 GENERAL INFORMATION:

APPLICANT: Taylor, Ronald K.
APPLICANT: LaPointe, Christian F.
APPLICANT: Trustees of Dartmouth

APPLICANT: Trustees of Dartmouth College
TITLE OF INVENTION: COMPOUNDS AND METHODS OF IDENTIFYING COMPOUNDS WHICH

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TELECOMMUNICATION: TELEPHONE: (703)836-9300
TELEPAX: (703)883-4109
TELEYAR: 899140
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IMMEDIATE SOURCE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: EP 9
FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION: 435
PRIOR APPLICATION DATA
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COMPUTER: IE
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TYPE: nucleic acid
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                                                                                   CTAAAGCAAGTTTTGTATAATTCAAAATACTT 444
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US-09-949-016-15328
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; LOCATION: (1).T.(111235; OTHER INFORMATION: n = US-09-949-016-15328
                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
PRIOR FILING DATE: 2000-09-08
                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
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Best Local
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SEQ ID NO 1
                                                                                                                                   SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 15328 LENGTH: 111235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 15328, Application US/09949016 Patent No. 6812339
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CURRENT FILING DATE: 2002-05-03
PRIOR APPLICATION NUMBER: 60/143,355
PRIOR FILING DATE: 1999-07-12
NUMBER OF SEQ ID NOS: 4
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                                                                                              ORGANISM: Human
                                                                                                                     TYPE: DNA
                                                         NAME/KEY: misc_feature
                                                                                FEATURE:
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Pred. No.
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Query Match

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US-09-949-016-13214
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US-09-949-016-13214/c
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APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: FastSEQ for Windows SEQ ID NO 13214
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Matches 67; Conserv
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                                                                                                                                                                                                                                            GENERAL INFORMATION:
                                                                                                                                                                                                                                                               Sequence 1, Application US/09790988 Patent No. 6632935
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Best Local :
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                                                             APPLICANT: SHIGENOBU, SHUJI
APPLICANT: WATANABE, HIDEMI
APPLICANT: WATANABE, HIDEMI
APPLICANT: HATTORI, MASAHIRA
APPLICANT: SAKAKI, YOSHIYUKI
TITLE OF INVENTION: GENOME DNA OF BACTERIAL SYMBIONT OF APHIDS
FILE REFERENCE: 081366/0159
CURRENT APPLICATION NUMBER: US/09/790,988
CURRENT PILING DATE: 2001-02-23
PRIOR APPLICATION NUMBER: JP2000-107160
PRIOR FILING DATE: 2000-04-07
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PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
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CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
                                NUMBER OF SEQ ID NOS: 7
SOFTWARE: PatentIn Ver. 2.1
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LENGTH: 640681
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0; Mismatches
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; ORGANISM: B:
US-09-790-988-1
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US-09-751-389-3
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US-09-248-796A-1989/c
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Patent No. 6630334
GENERAL INFORMATION:
Sequence 1989, Application US/09248796A
Patent No. 6747137
GENERAL INFORMATION:
APPLICANT: Keith Weinstock et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.132
CURRENT APPLICATION NUMBER: US/09/248,796A
CURRENT FILING DATE: 1999-02-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQ ID NOS: 8
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 3
                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 78; Conserv
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TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
TITLE OF INVENTION: THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/09/751,389
CURRENT FILING DATE: 2001-01-02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILE REFERENCE: CL001067
                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: misc_feature
LOCATION: (1)...(786431)
OTHER INFORMATION: n = A,T,C or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Human FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 786431
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SEQ ID NO 486
LENGTH: 564
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SEQ ID NO 1989
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: US 60/074,725
PRIOR FILING DATE: 1998-02-13
PRIOR APPLICATION NUMBER: US 60/096,409
PRIOR FILING DATE: 1998-08-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA ORGANISM: Candida albicans
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       329 ACATATACAAGGTTGTCGTGCTGAAATTTTTGGCTTGCTAACATCAAAGATGTATAC
                                                                                                                          57;
                                                                                                                                      Similarity
                         CTGTGGCATTTCCAATTTATATTCCCC 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ACCGATTGAATCTTCACTTGTTCGAGTTTTTGTCTTTTTGCTTCTAAAGGTCTTCAATTT 410
    CTTGGGCATATTTATAGCAACTTTACC 445
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Pred. No. 1.
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Pred. No. 1.1;
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111 GGTATTTTAACACACCTTAGAACTAAAACTTAATAATAATATTTTCTCTATCTTTAAAG
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TTGTCTCTGATACCAGCATTGTTGATCAAAATATTAATCCATGTGTTCTTGGAGTTTAAC
                                                                           CTGTGGCATTTCCAATTTATATTCCCCCTATTGGGTATTTGATGTGGCCGTTTAAATAGTC 350
                                                                                                                                                                                                                                                                                                                                                                                                   GCACATATTACGTGGCTAAGGCAATTACAGCTGATATACTGTAAAACTCATGTCGCCACT
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US-09-248-796A-486/c
US-09-248-796A-486/c
US-09-248-796A-486/c
Sequence 486, Application US/09248796A
; Patent NO. 6747137
; GENERAL INFORMATION:
APPLICANT: Keith Weinstock et al
; TITLE OF INVENTION: FOR DIAGNOSTICS AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; CURRENT FILING DATE: 1999-02-12
pRIOR APPLICATION NUMBER: US 60/074,725
pRIOR APPLICATION NUMBER: US 60/096,409
pRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION DATE: 1998-08-13
; PRIOR FILING DATE: 1998-08-13
AAATTCTTGTAGGGCCAGCTCGGTATCTTCCCATGGAACACCGAATATCCCCAGCATTGAT
                                                              AAATTCTTCTAACACGCGTTCTGTCTCTTTCCAAGGGACTCCGAATATGCCACTATTTAT 290
                                                                                                                                    30;
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472
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US-09-949-016-14810/c

US-09-949-016-14810, Application US/09949016

Patent No. 6812339

PARENTAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

ITITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT APPLICATION NUMBER: 00/04-14

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR FILING DATE: 2000-10-20

PRIOR PILING DATE: 2000-10-03

PRIOR APPLICATION NUMBER: 60/237,768

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: PASTUSE OF Windows Version 4.0

SEQ ID NO 14810

LENGTH: 174170

TYPE: DNA

CREANISM: Human

FEATURE:

NAME / KEY: misc feature

COCATION: (1) - (174170)

OTHER INFORMATION: n = A,T,C or G

US-09-949-016-14810
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Search completed: December 28, 2005, 11:18:48
Job time : 163 secs
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                                                                                                     170108
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                                                                                                                               159 CTATCTTTAAAGGCA 173
                                                                                                                                                                                                                                    99 ATTTATTTGAGAGGTATTTTAACACACCCTTAGAACTTAAAACTTAATAATAATAATTTTCT 158
                                                                                                                                                                                                                                                                                                                                    39 ACAGTATGAAAATATTTTTACTGTGATACTTACAAGTTGATATATGGTTGTGTGTAACTT 98
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Maximum DB seq length: 200000000
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Perfect score:
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Published_Applications_NA_Main:*

1: /cgn2_6/ptodata1/1/pubpna/USO7_PUBCOMB.seq:*

2: /cgn2_6/ptodata1/1/pubpna/USO8_PUBCOMB.seq:*

3: /cgn2_6/ptodata1/1/pubpna/USO9A_PUBCOMB.seq:*

4: /cgn2_6/ptodata1/1/pubpna/USO9A_PUBCOMB.seq:*

5: /cgn2_6/ptodata1/1/pubpna/US10A_PUBCOMB.seq:*

6: /cgn2_6/ptodata1/1/pubpna/US10B_PUBCOMB.seq:*

7: /cgn2_6/ptodata1/1/pubpna/US10B_PUBCOMB.seq:*

8: /cgn2_6/ptodata1/1/pubpna/US10B_PUBCOMB.seq:*

9: /cgn2_6/ptodata1/1/pubpna/US10B_PUBCOMB.seq:*

10: /cgn2_6/ptodata1/1/pubpna/US10B_PUBCOMB.seq:*
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Listing first 45 summaries
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Copyright (c) 1993 - 2005 Compugen Ltd.
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41.2	41.6	41.6	42	42.2	42.2	42.6	43.4	43.8	44.4	44.4	44.4	44.4	44.8	45	46.2	46.2	46.4	46.4	47	47	474.8	485	Score	
8.5	8.6	8.6	8.7	8.7	8.7	8.8	8.9	9.0	9.2	9.2	9.2	9.2	9.2	9.3	9.5	9.5	9.6	9.6	9.7	9.7	97.9	100.0	Match	Query
1230	6801	6801	14615	609	609	661	655	1803	517	517	517	517	7201	37515	6092	5739	1223197	122319	3254	3254	4046	485	Match Length	
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US-09-925-065A-77681	US-10-240-589C-100	US-10-311-455-1902	US-10-221-714A-429	US-10-027-632-208958	US-10-027-632-208958	US-09-925-065A-880535	US-09-925-065A-403939	US-09-925-065A-53227	US-10-363-483A-1844	US-10-363-483A-1843	US-10-363-345A-1844	US-10-363-345A-1843	US-10-311-455-309	US-10-433-793-28	US-10-221-613-36	US-10-311-455-691	US-10-027-632-179264	US-10-027-632-179264	US-10-027-632-114994	US-10-027-632-114994	US-10-600-230-81	US-10-600-230-1	ID	!
Sequence 77681, A	Sequence 100, App	Sequence 1902, Ap	Sequence 429, App		Sequence 208958,	Sequence 880535,	Sequence 403939,	Sequence 53227, A	Sequence 1844, Ap	Sequence 1843, Ap	Sequence 1844, Ap	Sequence 1843, Ap	Sequence 309, App	Sequence 28, Appl	Sequence 36, Appl	Sequence 691, App	Sequence 179264,	Sequence 179264,	Sequence 114994,	Sequence 114994,	Sequence 81, Appl	Sequence 1, Appli	Description	•

25 41.2 8.5 99472 8 US-10-464-577-673 26 41.2 8.5 109730 8 US-10-444-577-681 27 41.2 8.5 12893 8 US-10-484-577-681 28 41.2 8.5 12893 8 US-10-484-577-681 28 41.2 8.5 12893 8 US-10-484-577-681 29 41.2 8.5 172637 10 US-11-055-073-3 30 41 8.5 794 4 US-11-057-625-97 41 8.5 5443 8 US-10-857-625-97 32 41 8.5 5443 8 US-10-857-625-97 33 40.8 8.4 6223 7 US-10-221-613-13-5 34 40.8 8.4 3673778 6 US-10-221-631-1 35 40.6 8.4 535 4 US-09-925-065A-621748 36 40.6 8.4 551 4 US-09-925-065A-54823 37 40.6 8.4 551 4 US-09-925-065A-54823 38 40.6 8.4 888 5 US-10-027-632-135302 39 40.6 8.4 888 5 US-10-027-632-135302 40 40.6 8.4 888 6 US-10-027-632-135302 41 40.6 8.4 888 6 US-10-027-632-135303 42 40.6 8.4 888 6 US-10-027-632-135303 43 40.6 8.4 888 6 US-10-027-632-135303 44 40.6 8.4 888 6 US-10-027-632-135303 45 40.6 8.4 83391 7 US-10-231-714A-554 46 40.4 83391 7 US-10-231-714A-554 47 40.4 8.3 585 4 US-09-925-065A-557010
8.5 98472 8.5 128973 8.5 172637 8.5 172637 10 8.5 172637 10 8.5 172637 10 8.5 5443 8.4 6223 705 1 8.4 3673778 8.4 3673778 8.4 3673778 8.4 888 8.4 888
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28888 C 1 4 4 4 4 B B B B B B B B B B B B B B B
8 US-10-484-577-673 8 US-10-484-577-681 8 US-10-484-577-681 8 US-10-484-577-681 8 US-10-484-577-681 9 US-09-805-458A-3 10 US-11-055-073-3 10 US-11-071-972-1 10 US-11-071-972-1 10 US-10-857-625-97 10 US-10-312-841-1 10 US-09-925-065A-621748 10 US-09-925-065A-54823 10 US-09-925-065A-5549
US-10-484-577-673 US-10-484-577-673 US-10-484-577-681 US-09-805-458A-3 US-11-055-053-65323 US-11-057-625-97 US-10-857-625-97 US-10-221-613-115 US-09-925-065A-621748 US-09-925-065A-28494 US-09-925-065A-238494 US-09-925-065A-238493 US-10-027-632-135303 US-110-027-632-135303 US-10-027-632-135303

## ALIGNMENTS

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APPLICANT: WIRKINSON, Jack
APPLICANT: WIRKINSON, Jack
APPLICANT: WIRKINSON, Jack
APPLICANT: WIRKINSON, Jack
APPLICANT: Bertain, Sean
ITITLE OF INVENTION: GENETIC CONSTRUCTS HAVING HETEROLOGOUS
ITITLE OF INVENTION: 3' POLYADENYLATION SIGNAL SEQUENCE MOTIFS THAT FUNCTION IN
ITITLE OF INVENTION: PLANTS
ITITLE OF INVENTION: PLANTS
ITITLE OF INVENTION: PLANTS
ITITLE OF INVENTION NUMBER: US/10/600,230
CURRENT APPLICATION NUMBER: US/10/600,230
CURRENT APPLICATION NUMBER: 60/390,529
PRIOR APPLICATION NUMBER: 60/390,529
PRIOR FILING DATE: 2002-06-20
NUMBER OF SEQ ID NOS: 81
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1
LENGTH: 485
TYPE: DNA
ORGANISM: Saccharomyces cerevisiae
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                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 100.0%; Score 485; DB 7; Length 485; Best Local Similarity 100.0%; Pred. No. 7.1e-104; Matches 485; Conservative 0; Mismatches 0; Indels
241 AACACGCGTTCTGTCTCTTTCCAAGGGACTCCGAATATGCCACTATTTATCTGTGGCATT
                                                                                       181 CGTGGCTAAGGCAATTACAGCTGATATACTGTAAAACTCATGTCGCCCACTAAATTCTTCT
                                                                                                                                                   121 CACACCTTAGAACTAAAACTTAATAAATAATATTTCTCTATCTTTAAAGGCACATATTA
                                                                                                                                                                         121 CACACCTTAGAACTTAAAACTTAATAAATAATATTTCTCTATCTTTTAAAGGCACATATTA
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RESULT 2
US-10-600-230-81
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Publication No. US20040092020A1
GENERAL INFORMATION:
APPLICANT: Wilkinson, Jack
APPLICANT: McBride, Kevin
APPLICANT: Bertain, Sean
TITLE OF INVENTION: GENETIC CONSTRUCTS HAVING HETEROLOGOUS
TITLE OF INVENTION: JACANES
TITLE REFERENCE: 0325.210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/10/600,230
CURRENT FILING DATE: 2003-06-20
PRIOR APPLICATION NUMBER: 60/390,529
PRIOR FILING DATE: 2002-06-20
NUMBER OF SEQ ID NOS: 81
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
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Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              tch 97.9%; al Similarity 99.6%; 476; Conservative
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   ACTTGTTCGAGTTTTGTCTTTTGCTTCTCTAAAGGTCTTCAATTTTATCTAAAGCAAGTTT
                                                                                                                                                                   GCGTTCTGTCTCTTTCCAAGGGACTCCGAATATGCCACTATTTATCTGTGGCATTTCCAA 305
                                                                                                                                                                                                                                         CTAAGGCAATTACAGCTGATATACTGTAAAACTCATGTCGCCACTAAATTCTTCTAACAC
                                                                                                                                                                                                                                                                               CTTAGAACTAAAAATAATAAATATTTCTCTATCTTTAAAGGCACATATTACGTGG
                                                                                               TTTATATTCCCCTATTGGGTATTTGATGTGGCCGTTTAAATAGTCACCGATTGAATCTTC
                                                                                                                                 GCGTTCTGTCTCTTTCCAAGGGACTCCGAATATGCCACTATTTATCTGTGGCATTTCCAA
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Pred. No. 3.8e-101;
0; Mismatches 2;
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Sequence 114994, Application US/10027632

Publication No. US20030204075A9

GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
FILE REFERENCE: 108827.129

CURRENT APPLICATION NUMBER: US/10/027,632

CURRENT FILING DATE: 2002-04-30

PRIOR APPLICATION NUMBER: US 60/218,006

PRIOR APPLICATION NUMBER: US 60/198,676

PRIOR FILING DATE: 2000-07-12

PRIOR FILING DATE: 2000-04-20

PRIOR APPLICATION NUMBER: US 60/193,483
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RESULT 3
US-10-027-632-114994/c
Sequence 114994, Application US/10027632
Publication No. US20020198371A1
GENERAL INFORMATION:
APPLICANT: Wang, David G.
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PRIOR FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR FILING DATE: 2000-04-20
PRIOR PELLING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR PELLING DATE: 2000-03-29
PRIOR PELLING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR FILING DATE: 1000-02-24
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR APPLICATION NUMBER: US 60/146,002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR FILING DATE: 1999-08-09
NUMBER OF SEQ ID NOS: 325720
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 114994
LENGTH: 3254
                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
Matches 92; Conserv
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TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
FILE REFERENCE: 108827.129
CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
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                                    TTATCTAAAGCAAGTTTTGTATAATTCAAAATACTTTTGCTTTTCTCC 455
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                                                                                                                                                                  TCACCGATTGAATCTTCACTTGTTCGAGTTTTGTCTTTTGCTTCTAAAGGTCTTCAAT 408
                                                                                                                                                                                                                              ATCTTTAATTTAGATAATGTATTTTTTACTTCTAGAATTTTAATTTTGGCTCTTTTTAAAG
                                                                                                                                                                                                                                                                              ATCTGTGGCATTTCCAATTTATATTCCCCTATTGGGTATTTGATGTGGCCGTTTAAATAG
TTATTTAAAGATCTTGTATGTTAATTCTATATGTGTAGTTTTGCTTC
                                                                                                            TCTTCATTTCTATGCTGAAATTCTCCATCTTTTTCTCTAAATTCTTTAAAATGTTATGAT
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55.1%;
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Pred. No. 1.1;
0; Mismatches
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PRIOR FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR FILING DATE: 2000-02-24

APPLICATION NUMBER: US 60/167,363 FILING DATE: 1999-11-23

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US-10-027-632-114994
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                                                                                                                                                                                                        SOFTWARE: FastSEQ
SEQ ID NO 179264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
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Best Local Similarity
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                Query Match
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PRIOR
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CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/218,006
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: US 60/167,363 PRIOR FILING DATE: 1999-11-23
                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR FILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR FILING DATE: 2000-03-29
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                                                                                                                                                                                                                                              NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                              PRIOR FILING DATE: 2000-02-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR FILING DATE: 2000-07-12 PRIOR APPLICATION NUMBER: US 60/198,676
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                                                                                                                                                                                                                                                                    PRIOR FILING DATE:
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                                                                      NAME/KEY: misc_feature
LOCATION: (1)...(1223197)
OTHER INFORMATION: n = A,
                                                                                                                                                ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 3254
                                                                                                                                                                                          LENGTH: 1223197
Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US 60/156,358 FILING DATE: 1999-09-28 APPLICATION NUMBER: US 60/146,002
                                                                                                                                                                                                                                                                                  FILING DATE: 1999-09-28
APPLICATION NUMBER: US 60/146,002
                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US 60/156,358
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9.6%;
                                                                      A,T,C or
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Pred. No. 1.1;
0; Mismatches 7
Score 46.4;
Pred. No. 1:
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13;
                  DB 5;
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US-10-027-632-179264/c
                                                                              US-10-027-632-179264
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PRIOR FILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR FILING DATE: 1999-11-23
PRIOR FILING DATE: 1999-11-23
                                                                                                                                                                                                            NUMBER OF SEQ ID NOS:
SOFTWARE: FastSEQ for
SEQ ID NO 179264
LENGTH: 1223197
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    Matches
                    Best Local Similarity
                                      Query Match
                                                                                             TYPE: DNA
ORGANISM: Human
FEATURE:
NAME/KEY: misc feature
LOCATION: (1)...(1223197)
OTHER INFORMATION: n = A,T,C o:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
FILE REFERENCE: 108827.129
                                                                                                                                                                                                                                                                                           PRIOR FILING DATE: 1999-08-09
                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR FILING DATE: 1999-09-28
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                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US 60/146,002
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    Conservative
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9.6%; Score 46.4; I
28.0%; Pred. No. 13;
tive 86; Mismatches
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                                      DB 6;
    182;
                                        Length 1223197;
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US-10-311-455-691
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; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-311-455-691
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PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: DE 10043826.1
PRIOR FILING DATE: 2000-09-01
NUMBER OF SEQ ID NOS: 2424
SEQ ID NO 691
LENGTH: 5739
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                                                                                                                                                                                                                             Matches 194;
                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: PIEPENBROCK, Christian
APPLICANT: BERLIN, Kurt
TITLE OF INVENTION: Diagnosis of Diseases Associated with the Immune System by Determ
TITLE OF INVENTION: Cytosine methylation
FILE REFERENCE: 5013.1014
CURRENT APPLICATION NUMBER: US/10/311,455
CURRENT FILING DATE: 2002-12-16
PRIOR APPLICATION NUMBER: PCT/EP01/07537
PRIOR FILING DATE: 2001-07-02
PRIOR FILING DATE: 2001-07-02
PRIOR FILING DATE: 2001-07-02
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                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA
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GTAAAACTCATGTCGCCACTAAAATTCTTCTAACACGCGTTCTGTCTCTTTCCAAGGGACT 270
                                                                                                                             AATACTTTGCTT
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                                                              ATATTTCTCTATCTTAAAGGCACATATTACGTGGCTAAGGCAATTACAGCTGATATACT
                                Conservative
                                                                                                                                                                                                                                          9.5%;
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                                                                                                                                                                                                                                            Score 46.2; DE 
Pred. No. 2.1;
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                                                                                                                                                                                                                                                                                                                                                                   2000-09-01
; NUMBER OF SEQ ID NOS: 428
; SEQ ID NO 36
; LENGTH: 6092
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
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Publication No. US20040029123A1
GENERAL INFORMATION:
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DE 10043826.1

PRIOR FILING DATE: 2000-03-15
                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                              Matches 181;
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CURRENT FILING DATE: 2002-09-13
PRIOR APPLICATION NUMBER: PCT/EP01/02945
DE 10019847.00
DE 10019058.8
DE 10019173.8
DE 10019173.8
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TITLE OF INVENTION: Diagnosis of Diseases Associated with Cell Cycle
FILE REFERENCE: 5013.1004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2000-04-06 2000-04-07
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                                                                                                                                                                             122 ACACCTTAGAACTTAAAATAATAATATTTCTCTATCTTAAAGGCACATATTAC 181
                                                                                                                                                                                                                                              TTTTATATAAATTTTTTTGTTAGTTATTTTTTTTTGTGTACGTTTTAAAAATGTTTGTATG 1027
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               TGTTGTATTTTTATAATTTATAATAGTAATAAAATATGA---TAATTATTTGTGTGAAAT
                                                                              GTGGCTAAGGCAATTACAGCTGATATACTGTAAAACTCATGTCGCCACTAAATTCTTCTA
                                                                                                                                                ÁTTTTGTTTTÁATÁTÁTÁTTTGTGÁÁÁTÁTTTÁGTTTTTÁTTATTÁÁAGGTTTTGAÁTTÁT 5063
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                                            ACACGCGTTCTGTCTCTTTCCAAGGGACTCCGAATATGCCACTATTTATCTGTGGCATTT 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PIEPENBROCK, Christian
                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2001-03-15
                                                                                                                                                                                                                                                                                             9.5%;
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Pred. No. 2.1;
                                                                                                                                                                                                                                                                              Mismatches
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                                                                                                                                                                                                                                                                            203;
                                                                                                                                                                                                                                                                                                             Length 6092;
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5003

5123 241

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Sequence 309, Application US/10311455
; Publication No. US20030143606A1
; GENERAL INFORMATION:
   APPLICANT: OLEK, Alexander
; APPLICANT: PIEPENBROCK, Christian
APPLICANT: BERLIN, Kurt
; TITLE OF INVENTION: Diagnosis of Diseases Associated with the Imm.
; TITLE OF INVENTION: cytosine methylation
; TITLE OF INVENTION: UNUMBER: US/10/311,455
; CURRENT APPLICATION NUMBER: US/10/311,455
; CURRENT FILING DATE: 2002-012-16
; PRIOR APPLICATION NUMBER: DE 10032529.7
; PRIOR APPLICATION NUMBER: DE 10032529.7
; PRIOR APPLICATION NUMBER: DE 10043826.1
; PRIOR APPLICATION NUMBER: DE 10043826.1
; PRIOR APPLICATION NUMBER: DE 10043826.1
; PRIOR FILING DATE: 2000-06-30
pRIOR APPLICATION NUMBER: DE 10043826.1
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US-10-433-793-28
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US-10-311-455-309
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Best Local S
Matches 96
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CURRENT FILING DATE: 2003-06-06
NUMBER OF SEQ ID NOS: 212
SEQ ID NO 28
LENGTH: 37515
TYPE: DNA
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Publication No. US20040142334A1
GENERAL INFORMATION:
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TITLE OF INVENTION: Diagnose von mit Angiogenese assoziierten Krankheiten
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                                                                                                                                                                                                                                                                                                                                                                                                                                  CTTTAAAGGCACATATTACGTGGCTAAGGCAATTACAGCTGATATACTGTAAAACTCATG
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US-10-311-455-309
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TYPE: DNA
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Matches
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SEQ ID NO 1843
LENGTH: 517
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APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILE REFERENCE: E01/1227
CURRENT APPLICATION NUMBER: US/10/363,345A
CURRENT FILING DATE: 2003-03-03
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Artificial Sequence FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA
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Local Similarity 53.4%;
hes 94; Conservative
                                                                                                                                                                                                                                                                                                                                                      Local Similarity
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                                                           284 TATTTATCTGTGGCATTTCCAATTTATATTCCCCTATTGGGTATTTGATGTGGCCGTTTA 343
                                                                                          174;
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                                                                                                                                                                                                                                                                                                           44 ATGAAAATATTTTTACTGTGATACTTACAAGTTGATATATGGTTGTGTGTAACTTATTTA 103
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AATAGTCACCGATTGAATCTTCACTTGTTCGAGTTTTGTCTTTTGCTTCTCTAAAGGTCT 403
                                                                                                                       CGCCACTAAATTCTTCTAACACGCGTTCTGTCTCTTTCCAAGGGACTCCGAATATGCCAC
                                                                                                                                                     TAAAACTTAATAAATAATATTTCTCTATCTTTAAAGGCACATATTACGTGGCTAA 189
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                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                      9.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                    treated genomic DNA (Homo sapiens) No: 1843
                                                                                                                                                                                                                                                                                                                                                                       DB 8;
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CURRENT APPLICATION NUMBER: US/10/363,345A
CURRENT FILING DATE: 2003-03-03
NUMBER OF SEQ ID NOS: 40712
SEQ ID NO 1844
LENGTH: 517
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Chemically treated genomic DNA
OTHER INFORMATION: Cpg-island No: 1844
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US-10-363-345A-1844/c
US-10-363-345A-1844/c
; Sequence 1844, Application US/10363345A
; Publication No. US20040234960A1
; GENERAL INFORMATION:
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US-10-363-483A-1843
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Sequence 1843, Application US/10363483A
Publication No. US20050064401A1
GENERAL INFORMATION:
APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
TITLE OF INVENTION: Diagnosis of illnes
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: Method for determining the degree of methylation of defined TITLE OF INVENTION: cytosines in genomic DNA in the sequence context of 5'-CpG-3 FILE REFERENCE: E01/1227
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APPLICANT: Christian Piej
APPLICANT: Kurt Berlin
OF INVENTION: Diagnosis of illnesses or predisposition to certain
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                                                                                                                                                                                                                                                       344 AATAGTCACCGATTGAATCTTCACTTGTTCGAGTTTTGTCTTTTTGCTTCTCTAAAGGTCT
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                                                                                                                                                                   95
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Pred. No. 2.3;
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RESULT 14 US-10-363-483A-1844/c

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CURRENT FILING DATE: 2003-03-03
NUMBER OF SEQ ID NOS: 40712
SEQ ID NO 1843
LENGTH: 517
TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                               Matches 174; Conservative
                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION:
FILE REFERENCE: 82011
                                                                                                                                                                                                                                                                                                                                                                                                                              OTHER INFORMATION: chemically treated OTHER INFORMATION: CpG-island No: 1843
                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEATURE:
                                                                                                                                                                                                                                                                                                                                                                           Match 9.2%;
Local Similarity 44.6%;
                                                 363
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423
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 CGTTTTTTTTTACGTTATTTTTCGTTTAT
                        TCAATTTATCTAAAGCAAGTTTTGTATAAT 433
                                                                          AATAGTCACCGATTGAATCTTCACTTGTTCGAGTTTTTGTCTTTTGCTTCTCTAAAGGTCT
                                                                                                     TATTTATCTGTGGCATTTCCAATTTATATTCCCCCTATTGGGTATTTGATGTGGCCGTTTA 343
                                                                                                                                                       CGCCACTAAATTCTTCTAACACGCGTTCTGTCTCTTTCCAAGGGACTCCGAATATGCCAC 283
                                                                                                                                                                                                         TTTAAAGGCACATATTACGTGGCTAAGGCAATTACAGCTGATATACTGTAAAACTCATGT
                                                 illnesses
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Pred. No. 2.3;
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Sequence 1844, Application US/10363483A
Publication No. US20050064401A1
GENERAL INFORMATION:
APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
TITLE OF INVENTION: biagnosis of illnesses or
TITLE OF INVENTION: illnesses
FILE REFERENCE: 82011
CURRENT APPLICATION NUMBER: US/10/363,483A
CURRENT FILING DATE: 2003-03-03
NUMBER OF SEQ ID NOS: 40712
SEQ ID NO 1844
LENGTH: 517
TYPE: DNA
ORGANISM: Artificial Sequence
                                                                        ; FEATURE:
OTHER INFORMATION: chemically
OTHER INFORMATION: CpG-island
US-10-363-403A-1844
Query Match 9.2%;
Best Local Similarity 44.6%;
Matches 174; Conservative
 Score 44.4; DB Pred. No. 2.3; 0; Mismatches
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                                                                                             treated genomic DNA No: 1844
                                      DB
   216;
                                      9;
                                      Length
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     Indels
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Sequence 53227, Application US/09925065A

PUDDICATION NO. US20050228172A9

GENERAL INFORMATION: US20050228172A9

GENERAL INFORMATION: Identification and Mapping of Single

FILLE OF INVENTION: Identification and Mapping of Single

FILLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome

FILLE REFERENCE: 108827.135

CURRENT FILING DATE: 2001-08-08

PRIOR APPLICATION NUMBER: US 60/243,096

PRIOR APPLICATION NUMBER: US 60/252,147

PRIOR FILING DATE: 2000-11-20

PRIOR APPLICATION NUMBER: US 60/252,147

PRIOR APPLICATION NUMBER: US 60/250,092

PRIOR APPLICATION NUMBER: US 60/261,766

PRIOR FILING DATE: 2001-01-16

PRIOR FILING DATE: 2001-01-16

PRIOR FILING DATE: 2001-03-09

VIMMER OF SECTION NUMBER: US 60/289,846
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; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 53227
; LENGTH: 1803
; TYPE: DNA
; ORGANLEM: Homo sapiens
US-09-925-065A-53227
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US-09-925-065A-53227
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168 AAGGCACATATTACGTGGCTAAGGCAATTACAGCTGATATACTGTAAAACTCATGTCGCC 227
                                                            189
                                                                                          129 AGAAATATGTTATTCTTCACCAGCAAGATGTTGGGTGGTAGTGTGTAATACATCTTTTAT
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Search completed: December 28, 2005, 11:32:43 Job time : 825 secs

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6381 Sequence 46381, A RESULT 2
3 Sequence 93, Appl US-10-240-708-62
6438 Sequence 36438, A ; Sequence 62, Application US/10240708
6438 Sequence 40, Appl ; Publication No. US20050282157A1
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Result
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Maximum Match 100%
Listing first 45 summaries
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Perfect score:
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1: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*

2: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*

3: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*

4: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*

5: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*

6: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*

7: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq:*

8: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq:*

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                                   40000000001101010
              US-11-121-086-79
US-10-240-708-62
US-10-240-708-62
US-10-270-185-50224
US-10-750-185-55780
US-10-750-185-55780
US-10-750-185-64497
US-10-121-086-39
US-11-121-086-39
US-11-121-086-39
US-10-750-185-30231
US-10-750-185-30231
US-10-750-185-30231
US-10-995-561-13443
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Sequence 60, Appl
Sequence 90, Appl
Sequence 188, Appl
Sequence 188, Appl
Sequence 84, Appl
Sequence 64, Appl
Sequence 64, Appl
Sequence 30, Appl
Sequence 73227, Appl
Sequence 30231, A
Sequence 30457, A
Sequence 13443, A
Sequence 13443, A
Sequence 13443, A
Sequence 1304, A
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                              Sequence
                        3 9, Appl
3 73227, Appl
3 73227, A
3 39457, A
2 13457, A
2 13304, A
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Sequence 3073, Ap Sequence 3340, Ap	Sequence 44880, A Sequence 13286, A	Sequence 38146, A	Sequence 13, Appl Sequence 13, Appl Sequence 13421, A	Sequence 211, App	Sequence 58341, A	Sequence 77, Appl Seguence 42981, A		Sequence 50592, A Sequence 58628, A	Sequence 15, Appl	50,52	Sequence 3453, Ap Sequence 13199, A

## ALIGNMENTS

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Query Match
Best Local Similarity
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SEQ ID NO 79
LENGTH: 177175
TYPE: DNA
ORGANISM: Homo sapiens
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US-11-121-086-79
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Publication No. US20050266459A1

GENERAL INFORMATION:
APPLICANT: POULSEN, TIM S.
APPLICANT: NIELSEN, KIRSTEN V.

TITLE OF INVENTION: NUCLEIC ACID PROBES AND NUCLEIC ACID ANALOG PROBES
FILE REFERENCE: 09138.6000-00000

CURRENT APPLICATION NUMBER: US/11/121,086

CURRENT FILING DATE: 2004-05-04

PRIOR APPLICATION NUMBER: 60/567,570

PRIOR APPLICATION NUMBER: 2004-05-04

NUMBER: 2004-05-04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQ ID NOS: 107
76790 TTTTAATTT
                                                                      76730 ATTCTAGATCTCATGATAATCTGTAACACTTCTTTTAACTCAATAGAAGTAATTCCTCTG
                                                                                                                                                                                                             76610 TCCTGCTACATATACATTTTTCAAAAACAGCTTGACTGTTATGCTTAAAATGTGATATAT
                                                                                                                                          76670 TATTTCATGTAATTTATATTCAATAAAATTAATCTAAAAAAGATTAATAAAAAGGATTTAG
                                   204 ATATACTGT 212
                                                                                                       144 TAAATAAATATTTCTCTATCTTTAAAGGCACATATTACGTGGCTAAGGCAATTACAGCTG
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                                                                                                                                                                                                                                                                                 8.6%;
ilarity 51.3%;
Conservative
 76798
                                                                                                                                                                                                                                                                                 Score 41.8; DB
Pred. No. 1.2;
0; Mismatches
                                                                                                                                                                                                                                                                                   0;
                                                                                                                                                                                                                                                                                                                      DB
                                                                                                                                                                                                                                                                                   92;
                                                                                                                                                                                                                                                                                                                     Length 177175;
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APPLICANT: OLEK, Alexander
APPLICANT: PIEPENBROCK, Christian
APPLICANT: PIEPENBROCK, Christian
APPLICANT: BERLIN, Kurt
ITILE OF INVENTION: Diagnosis of Diseases Associated with DNA Replication
ITILE OF INVENTION: Diagnosis of DNA Methylation
FILTE OF INVENTION: Dy Assessing DNA Methylation
FILTE REFERENCE: S013.1012
CURRENT APPLICATION NUMBER: US/10/240,708
CURRENT FILING DATE: 2002-10-03
PRIOR APPLICATION NUMBER: DE 10019071
PRIOR APPLICATION NUMBER: DE 10019058.8
PRIOR APPLICATION NUMBER: DE 10019058.8
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR APPLICATION NUMBER: DE 10032529.7
PRIOR APPLICATION NUMBER: DE 10032529.7
PRIOR APPLICATION NUMBER: DE 10032529.7
PRIOR APPLICATION NUMBER: DE 10043826.1
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION DATE: 2000-09-01
PRIOR FILING DATE: 2000-09-01
PRIOR FILING DATE: 2000-09-01
PRIOR FILING DATE: 2000-09-01
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                                                                                                                                                           US-11-121-086-90/c
Sequence 90, Application US/11121086
Publication No. US20050266459A1
GENERAL INFORMATION:
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LENGTH: 6801
TYPE: DNA
                                                                                                                                                                                                                                                           RESULT 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
                 APPLICANT: POULSEN, TIM S.
APPLICANT: NIELSEN, KIRSTEN V.
APPLICANT: NIELSEN, KIRSTEN V.
TITLE OF INVENTION: NUCLEIC ACID PROBES AND NUCLEIC ACID ANALOG
FILE REFERENCE: 09138.6000-00000
CURRENT APPLICATION NUMBER: US/11/121,086
CURRENT FILING DATE: 2005-05-04
PRIOR APPLICATION NUMBER: 60/567,570
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       300
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APPLICANT: BATES, Scephen
APPLICANT: PANTIN, Dennis
TITLE OF INVENTIN, Dennis
TITLE REFERENCE: MMILIO-2
CURRENT APPLICATION NUMBER: US/10/750,185
CURRENT FILING DATE: 2003-12-31
PRIOR APPLICATION NUMBER: US 60/437,482
PRIOR APPLICATION NUMBER: US 60/437,482
PRIOR FILING DATE: 2002-12-31
PRIOR FILING DATE: 2002-12-31
PRIOR FILING DATE: 2002-12-31
PRIOR FILING DATE: 2002-12-31
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                                                                                                           US-11-117-187-188/c
                                                                                                                           RESULT 5
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NUMBER OF SEQ ID NOS: 107
SOFTWARE: PatentIn version 3.3
SEQ ID NO 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 8.0%;
Best Local Similarity 52.5%;
Matches 85; Conservative
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LENGTH: 1303
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 50224, Application US/10750185 Publication No. US20050260603A1
Sequence 188, Application US/11117187
publication No. US20050266560A1
GENERAL INFORMATION:
APPLICANT: PREUSS, DAPHNE
APPLICANT: COPENHAVER, GREGORY
APPLICANT: COPENHAVER, GREGORY
TITLE OF INVENTION: PLANT ARTIFICIAL CHROMOSOME COMPOSITIONS AND METHODS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT:
                                                                                                                                                                                                                                                                                                                                                Query Match 7.8%;
Best Local Similarity 57.6%;
                                                                                                                                                                                                                                                                                                                               Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 148220
TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: PatentIN version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     17 AAGTGACTCCTTCGTTGCGTAGACAGTATGAAAATATTTTTACTGTGATACTTACAAGTT
                                                                                                                                                                                                                                                                                  351 ACCGATTGAATCTTCACTTGTTCGAGTTTTTGTCTTTTGCTTCTAAAGGTCTTCAATTT 410
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                                                                                                                                                                                                                                                                                                                               0;
                                                                                                                                                                                                                                                                                                                                                  Score 38; I
Pred. No. 2.
                                                                                                                                                                                                                                                                                                                                   Mismatches
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; Sequence 84, Application US/11121086
; Publication No. US20050266459A1
; GENERAL INFORMATION:
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; AAME/KEY: modified base
; LOCATION: (2720)...(72695)
; OTHER INFORMATION: N = A, C G, or T/U
US-11-117-187-188
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Best Local Similarity
""" hes 92; Conserva
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CURRENT APPLICATION NUMBER: US/11/117,187
CURRENT FILING DATE: 2005-04-28
PRIOR APPLICATION NUMBER: US/09/531,120
PRIOR FILING DATE: 2000-03-17
PRIOR APPLICATION NUMBER: 60/125,219
PRIOR FILING DATE: 1999-03-18
NUMBER OF SEQ ID NOS: 212
                                                                                                                                                                                                                                                                     SEQ ID NO 84
LENGTH: 118996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOPTWARE: PATENTIN Ver. 2.1
SEQ ID NO 188
LENGTH: 95223
                                                                                                                                               Matches
                                                                                                                                                          Query Match
Best Local Similarity
                                                                                                                                                                                                                  -11-121-086-84
                                                                                                                                                                                                                                                                                                                      APPLICANT: POULSEN, TIM S.
APPLICANT: NIELSEN, KIRSTEN V.
APPLICANT: NIELSEN, KIRSTEN V.
TITLE OP INVENTION: NUCLEIC ACID PROBES AND NUCLEIC ACID ANALOG PROBES
FILE REFERENCE: 09138.6000-00000
CURRENT APPLICATION NUMBER: US/11/121,086
CURRENT FILING DATE: 2005-05-04
PRIOR APPLICATION NUMBER: 60/567,570
PRIOR FILING DATE: 2004-05-04
NUMBER OF SEQ ID NOS: 107
                                                                                                                                                                                                                                                                                                       SOFTWARE: PatentIn version 3.3
                                                                                                                                                                                                                                   TYPE: DNA ORGANISM: Homo sapiens
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   9770
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GCCGTTTCAAATCTTTTCTGAAATAAACAAGATACACATAAAGGTGTAAAATGATGTCAT 9829
                                 TCTTTCTATATTCATTCTCATTTCTAAAGGTATGTGTCTGGGTTATTTTTACCCTTGTAA
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                                                                                                                                                          7.8%;
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                                                                                                                                           Score 38; DB 7; Length 118996; Pred. No. 8.9; 0; Mismatches 155; Indels 0
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APPLICANT: DeNISE, Sue K.

APPLICANT: KERR, Richard

APPLICANT: KERR, Richard

APPLICANT: HOLM, Tom

APPLICANT: HOLM, Tom

APPLICANT: BATES, Stephen

APPLICANT: FANTIN, Dennis

TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS

FILE REFERENCE: MMI1100-2

CURRENT APPLICATION NUMBER: US/10/750,185

CURRENT FILING DATE: 2003-12-31

PRIOR APPLICATION NUMBER: US 60/437,482

PRIOR APPLICATION NUMBER: US 60/437,482

PRIOR FILING DATE: 2002-12-31

NUMBER OF SEQ ID NOS: 64922

SOFTWARE: PATENTIN VETSION 3.1

SEQ ID NO 55780
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US-11-121-086-105
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 7
US-10-750-185-55780
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ś
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                                                                                Sequence 105, Application US/11121086

Publication No. US20050266459A1

GENERAL INFORMATION:

APPLICANT: POULSEN, TIM S.

APPLICANT: NIELSEN, KIRSTEN V.

APPLICANT: INVENTION: NUCLEIC ACID PROBES AND NUCLEIC ACID ANALOG PROBES

FILE REFERENCE: 09138.6000-00000

CURRENT APPLICATION NUMBER: US/11/121,086

CURRENT APPLICATION NUMBER: 05/57,570

PRIOR APPLICATION NUMBER: 60/567,570

PRIOR PILING DATE: 2004-05-04

NUMBER DE SECTION NUMBER: 2004-05-04
                     SOFTWARE: PatentIn version 3.3 SEQ ID NO 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: MMI GENOMICS, INC.
APPLICANT: DENISE, Sue K.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                   NUMBER OF SEQ ID NOS: 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA
LENGTH: 171486
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mes 77; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                114 ATTTTAACACACCTTAGAACTAAAACTTAATAAATAATATTTCTCTATCTTTAAAGGCA 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      174 CATATTACGTGGCTAAGGCAATT 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 54
                                                                                                                                                                                                                                                                                                                                                                                                                                             TTTATAAAATTTAAAATATAATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TTTTACTGTGATACTTACAAGTTGATATATGGTTGTGTGTAACTTATTTTGAGAGGT 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TTTTTCAAATAATGATATAAGGAAAGACATGATAAAATTTAAAAATATTTAATTTGAGGACT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GCACATATTACGTGGCTAAGGCAATTACAGCTGATATACTGTAAAACTCATGTCGCCACT 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CTGAAAAACTTCCATTGCCTAGTGACCTCATAGCCATAGTATGTGG 9995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATGTGCTTCATAATGACGTTTCAGTCAATGAAGTGGTGGTCCCATGAGATTACAATGGAG
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Pred. No. 2.7;
0; Mismatches 66;
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APPLICANT: FANTIN, Dennis
TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOY
FILE REFERENCE: MMILIO-2
CURRENT APPLICATION NUMBER: US/10/750,185
CURRENT FILING DATE: 2003-12-31
PRIOR APPLICATION NUMBER: US 60/437,482
PRIOR FILING DATE: 2002-12-31
PRIOR FILING DATE: 2002-12-31
NUMBER OF SEQ ID NOS: 64922
SOFTWARE: PATENTIN VERSION 3.1
SEQ ID NO 64497
LENGTH: 1150
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; ORGANISM: Homo sapiens
US-11-121-086-105
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US-10-750-185-64497
; Sequence 64497, Application US/10750185
; Publication No. US20050260603A1
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; ORGANISM: Bovine
US-10-750-185-64497
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US-11-121-086-39
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APPLICANT: MMI GENOMICS, INC.
APPLICANT: DENISE, Sue K.
APPLICANT: KERR, Richard
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Best Local Similarity
Sequence 39, Application US/11121086
Publication No. US20050266459A1
GENERAL INFORMATION:
APPLICANT: POULSEN, KIRSTEN V.
APPLICANT: NIELSEN, KIRSTEN V.
APPLICANT: NIELSEN, KIRSTEN V.
TITLE OF INVENTION: NUCLEIC ACID PROBES AND NUCLEIC ACID ANALOG PROBES
FILE REFERENCE: 09138.6000-00000
CURRENT APPLICATION NUMBER: US/11/121,086
CURRENT PILING DATE: 2005-05-04
PRIOR APPLICATION NUMBER: 60/567,570
PRIOR FILING DATE: 2004-05-04
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Best Local Similarity 58.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            82;
                                                                                                                                                                                                                                                                                  326 ATAATTTGTTTTTCTGAAGATTATTTGAAGGGATATCAGAAAAAATAAT 374
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                                                                                                                                                                                                                                                                                                                  GTAACTTATTTATTTGAGAGGTATTTTAACACACCTTAGAACTAAAACT 140
                                                                                                                                                                                                                                                                                                                                                       TACATTTAAAATGACAATATTAAATAAAGATAATCAAAAATTGATTTATCTTTGTTT
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HOLM, Tom
BATES, Stephen
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                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 37; DB 6; Length 1150; Pred. No. 3.9;
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NUMBER OF SEQ ID NOS: 107
SOFTWARE: PatentIn version 3.
SEQ ID NO 39
LENGTH: 207835
TYPE: DNA
ORGANISM: Homo sapiens
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US-11-121-086-40
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: PatentIn version 3.3 SEQ ID NO 40
                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 103; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: POULSEN, TIM S.
APPLICANT: NIELSEN, KIRSTEN V.
APPLICANT: NIELSEN, KIRSTEN V.
TITLE OP INVENTION: NUCLEIC ACID PROBES AND NUCLEIC ACID ANALOG PROBES
FILE REFERENCE: 09138.6000-00000
CURRENT APPLICATION NUMBER: US/11/121,086
CURRENT FILING DATE: 2005-05-04
PRIOR APPLICATION NUMBER: 60/567,570
PRIOR FILING DATE: 2004-05-04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQ ID NOS: 107
                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 207835
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                                                                                                                                                         199948 ССТТСААСААЛАТАЛААТСААТСТССТТААААТСААСАААТТАТСАТСААТТССТСААЛА
                                                                                                                                                                                                                                         199888 ATGTAAAATTTAATAAAATTTTAAATTTTAGATACATTTAAAATGTCAAAGTCCTCCTTAA 199947
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            138 ACTTAATAAATAATATTTCTCTATCTTTAAAGGCACATATTACGTGGCTAAGGCAATTA
                                                                                                                                                                                               138 АСТТААТАААТААТАТТТСТСТАТСТТТАААСССАСАТАТТАССТСССТААСССААТТА 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            78 ATATATGGTTGTGTGAACTTATTTATTTGAGAGGTATTTTAACACACCTTAGAACTAAA
                                                                                                                  198 CAGCTGATATACTGTAAAACTCATGTCGCCACTAAATTCTTCTAACACGCGTTCTGTCTC
                                                                                                                                                                                                                                                                            78 ATATATGGTTGTGTGTAACTTATTTATTTGAGAGGTATTTTAACACACCTTAGAACTAAA 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATATTTATATTGTGTTAACCTCATTTACCAAGACATTTCAAATTTACATCTTTGTGTCTG 200067
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TTTCCAAGGGACTCCGAATATGCCACTATTTAT 290
                                                                            ATATTTATATTGTGTTAACCTCATTTACCAAGACATTTCAAATTTACATCTTTGTGTCTG
                                     TTTCCAAGGGACTCCGAATATGCCACTATTTAT 290
TTAAAGACAGATTTAGAAATACACTAATTTTAT 200100
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                                                                                                                                                                                                                                                                                                                                            Score 37;
Pred. No. :
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                                                                                                                                                                                                                                                                                                                                                                 DB 7; Length 207835;
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US-10-995-561-73227/c

RESULT 12

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US-10-750-185-30231
                                                                                                                                                                                                                                                         ; ORGANISM: Bovine US-10-750-185-30231
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APPLICANT: CARGILL, Michele et al.

APPLICANT: CARGILL, Michele et al.

TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH

TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS (
TITLE OF INVENTION: DETECTION AND USES THEREOF

FILE REFERENCE: CL001559

CURRENT APPLICATION NUMBER: US/10/995,561

CURRENT APPLICATION NUMBER: US/10/995,561

CURRENT FILING DATE: 2004-11-24

NUMBER OF SEQ ID NOS: 85702

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 73227

LENGTH: 201

TYPE: DNA

COCCANUM USES THEREOF
                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/10/750,185
CURRENT FILING DATE: 2003-12-31
PRIOR APPLICATION NUMBER: US 60/437,482
PRIOR FILING DATE: 2002-12-31
NUMBER OF SEQ ID NOS: 64922
SOFTWARE: PatentIN version 3.1
SEQ ID NO 30231
LENGTH: 1048
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 30231, Application US/10750185 Publication No. US20050260603A1 GENERAL INFORMATION:
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Best Local 9
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Publication No. US20050272054A1
                                                                                                                                                                       Matches
                                                                                                                                                                                            Best Local Similarity
                                                                                                                                                                                                              Query Match
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APPLICANT: FANTIN, Dennis
TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
FILE REFERENCE: MMI1100-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: MMI GENOMICS,
APPLICANT: DeNISE, Sue I
APPLICANT: KERR, Richard
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                                                                                                                                                                                                                                                                                                    TYPE: DNA
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120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       69 TACAAGTTGATATATGGTTGTGTGTAACTTATTTATTTGAGAGGTATTTTAACACACCTT 128
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9 AAGGAGGAAAGTGACTCCTTCGTTGCGTAGACAGTATGAAAATATTTTTTACTGTGATACT
                                        AAATAGTCACCGATTGAATCTTCACTTGTTCGAGTTTTGTCTTTTGCTTCTCAAAGGTC 402
                                                                                                                            CTATTTATCTGTGGCATTTCCAATTTATATTCCCCCTATTGGGTATTTGATGTGGCCGTTT 342
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ACTCATTGCTCTATTTAAATTACACTTGGTCTTTTTGACAATTTTGTTTCATAACAATTA 179
                                                                                 CTCGCTCTTAGTGGCATTCCCTAGTCATCTTAACATTTTTCATATCTAAATTTAATAGAA 119
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KERR, Richard
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                                                                                                                                                                       Conservative
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Pred. No. 4.8;
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Pred. No. 2.9;
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Sequence 13443, Application US/10995561

Publication No. US20050272054A1

GENERAL INFORMATION:
APPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONTITLE OF INVENTION: DETECTION AND USES THEREOF FILE REFERENCE: CL001559

CURRENT APPLICATION NUMBER: US/10/995,561

CURRENT FILING DATE: 2004-11-24

NUMBER OF SEQ ID NOS: 85702

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 13443

LENGTH: 49979

TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: KERR, Richard
APPLICANT: ROSENFELD, David
APPLICANT: HOLM, Tom
APPLICANT: HOLM, Tom
APPLICANT: BATES, Stephen
APPLICANT: FANTIN, Dennis
TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
FILE REFERENCE: MMI1100-2
CURRENT APPLICATION NUMBER: US/10/750,185
CURRENT FILING DATE: 2003-12-31
PRIOR APPLICATION NUMBER: US 60/437,482
PRIOR FILING DATE: 2002-12-31
NUMBER OF SEQ ID NOS: 64922
SOFTWARE: PatentIN version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-10-750-185-39457; Sequence 39457, Application US/10750185; Publication No. US20050260603A1
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US-10-995-561-13443/c
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LENGTH: 1588
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: MMI GENOMICS, INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA
ORGANISM: Bovine
PEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(49979)
                                                                ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Match 7.5%;
Local Similarity 50.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1405 TAAAAAAAATAATAATTATTTGTATTTCATGAAAGAGATTTCTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11 GGAGGAAAGTGACTCCTTCGTTGCGTAGACAGTATGAAAATATTTTTACTGTGATACTTA 70
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Pred. No. 6.8;
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                                                                                                                                                                                                                                                                                          DRUG RESPONSE, METHODS
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## November 2005

Published\_Applications Nucleic Acid and Published\_Applications Amino Acid database searches now generate two sets of results each. The Published\_Applications databases have been split into two parts to reduce the amount of time required for their daily updates. This results in more machine time being available for processing searches.

Newly published applications will appear in the Published\_Applications\_New databases; older published applications make up the Published\_Applications\_Main databases.

Searches run against Nucleic Acid Published\_Applications produce two sets of results, with the extensions .rnpbm (Published\_Applications\_NA\_New).

Searches run against Amino Acid Published\_Applications produce two sets of results, with the extensions .rapbm (Published\_Applications\_AA\_New).

The POOR BIONA (USOIO)